

FIG. 1A

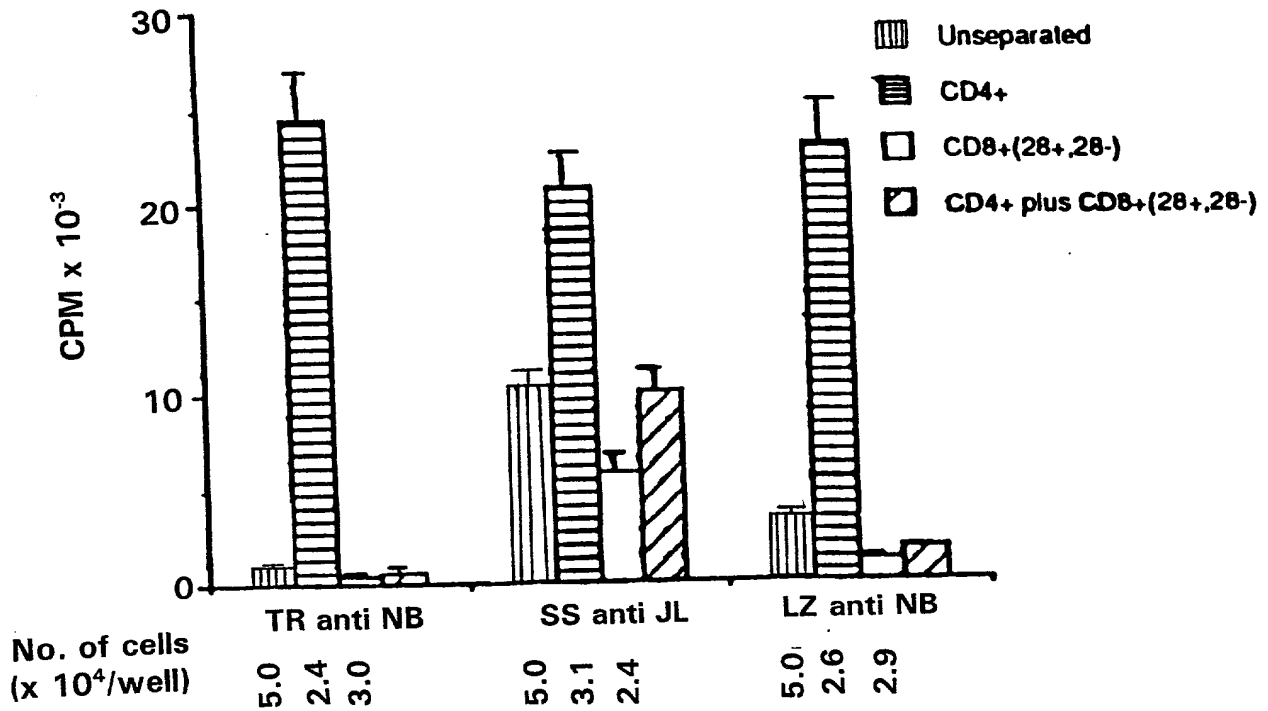


FIG. 1B

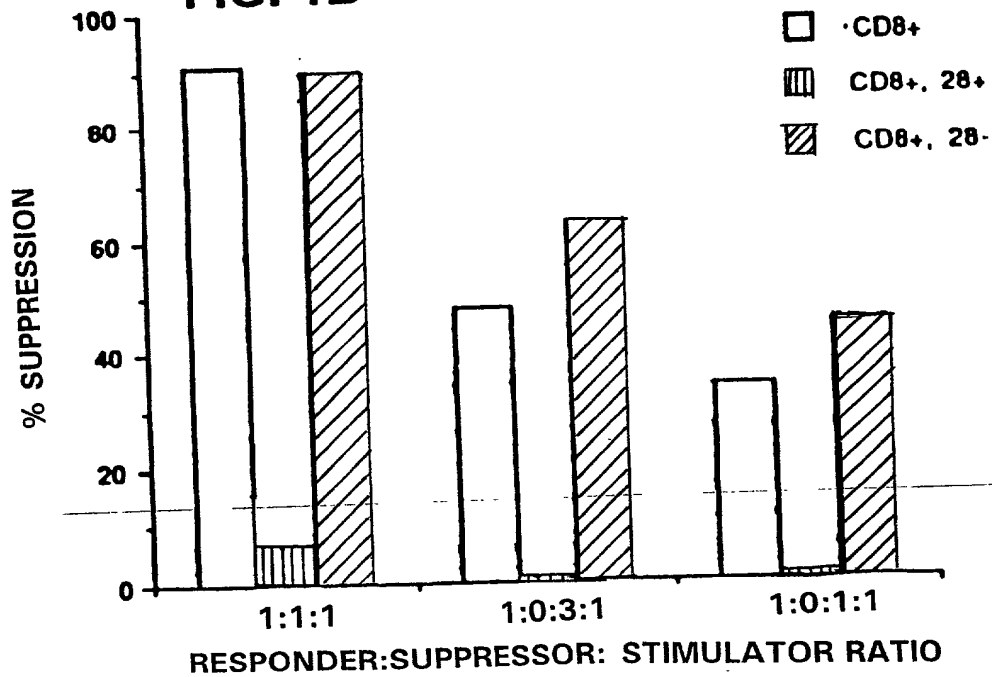


FIG. 1C

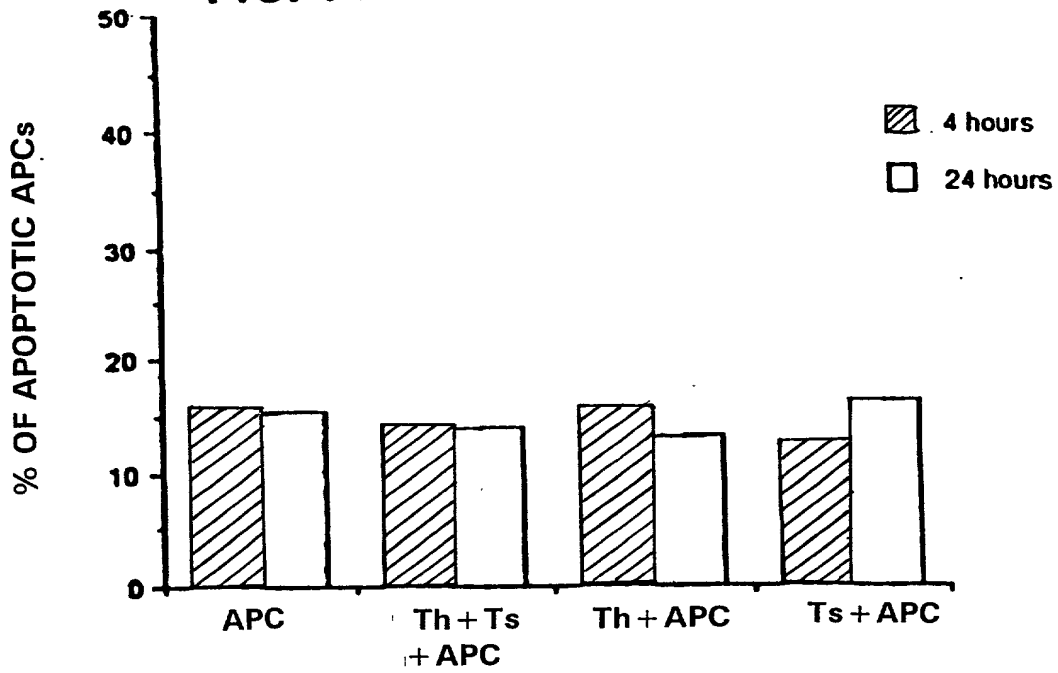


FIG. 1D

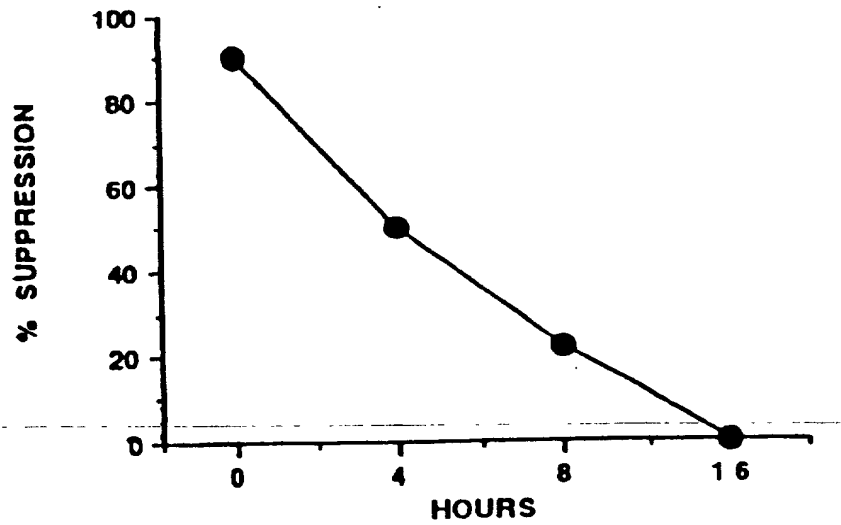


FIG. 2A

A

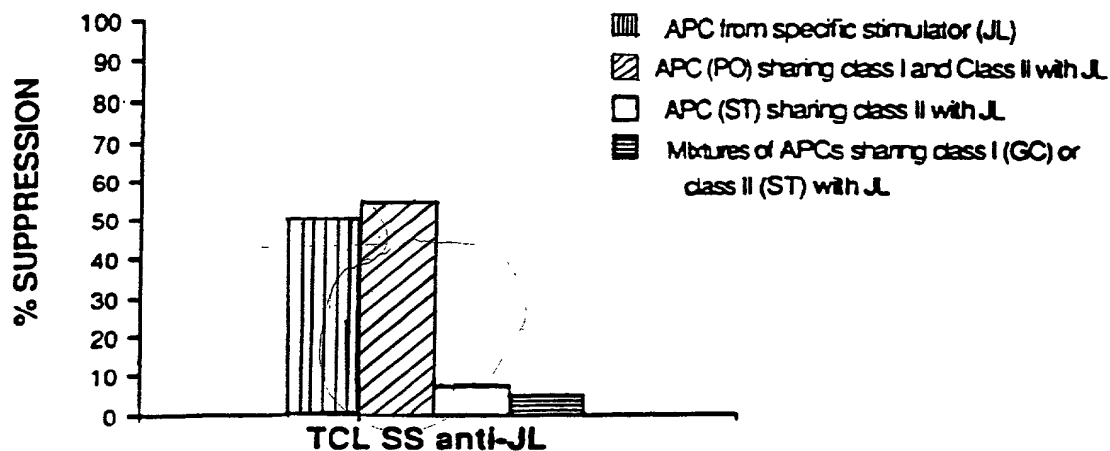


FIG. 2B

B

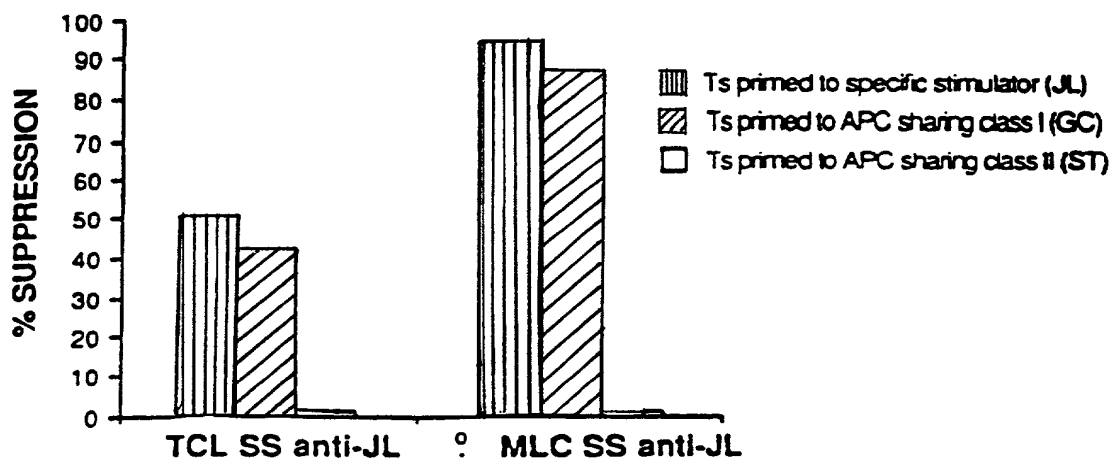
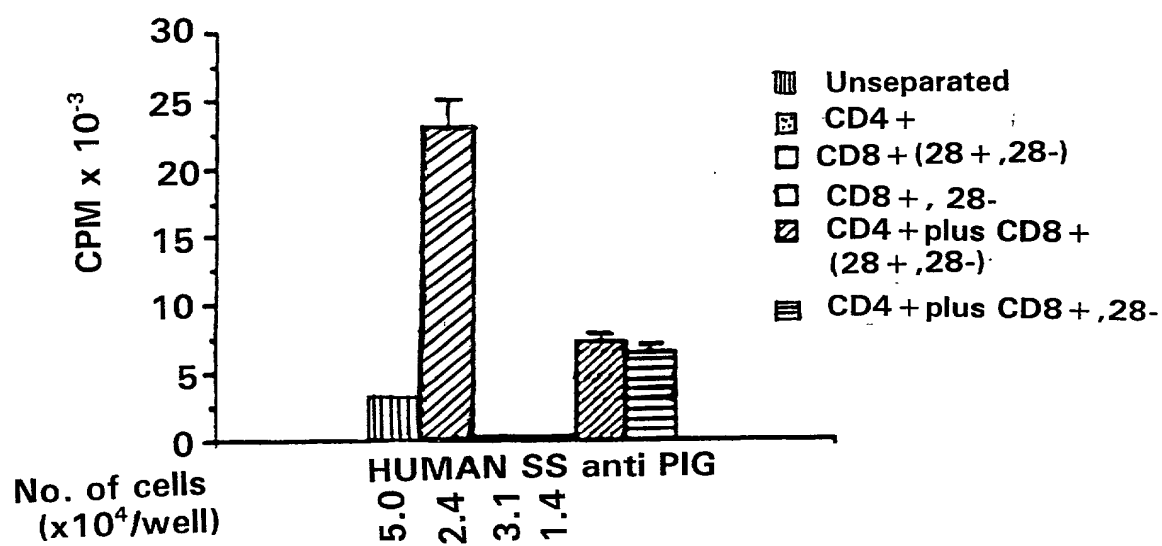


FIG. 3



5/73

FIG. 4A

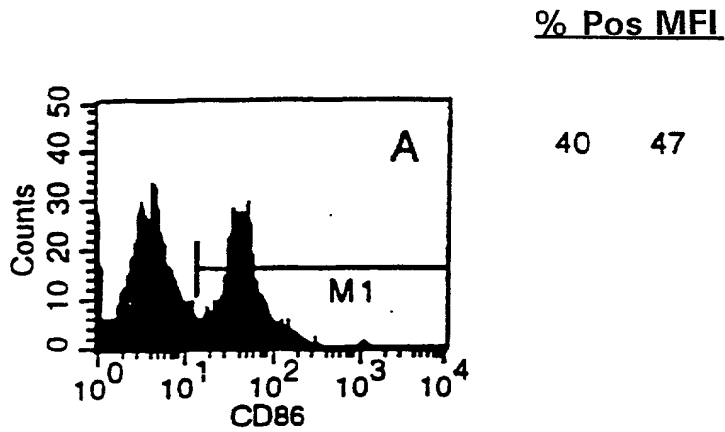


FIG. 4B

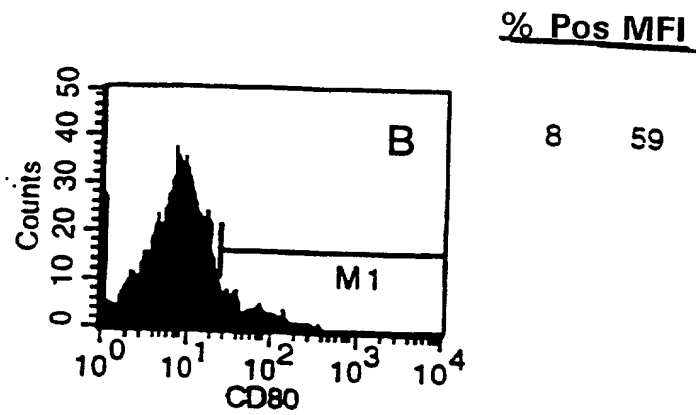


FIG. 4C

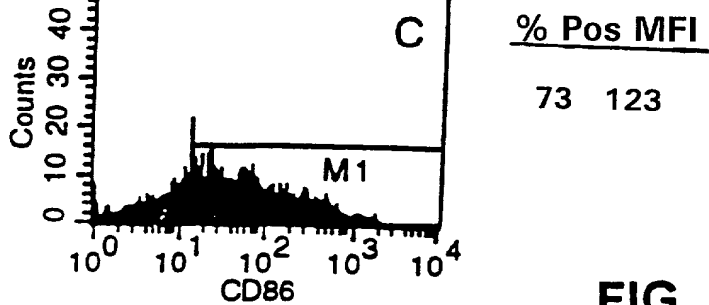
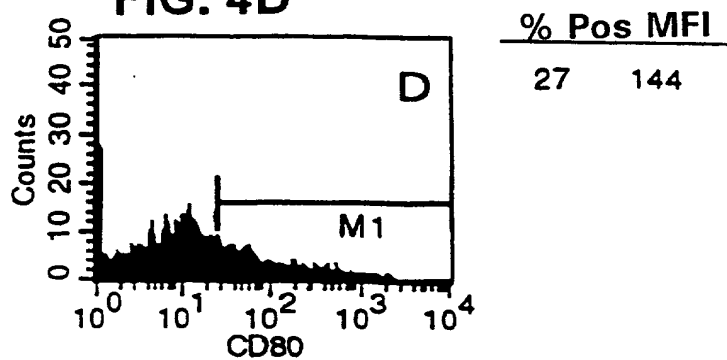


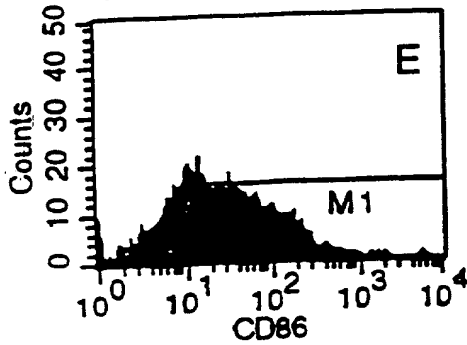
FIG. 4D



007227-TE3460

6/73

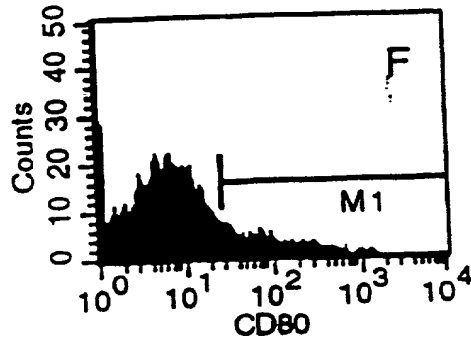
FIG. 4E



% Pos MFI

63 78

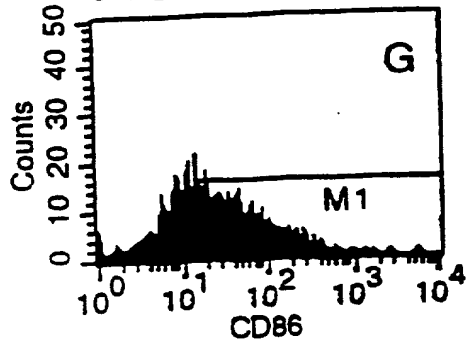
FIG. 4F



% Pos MFI

13 128

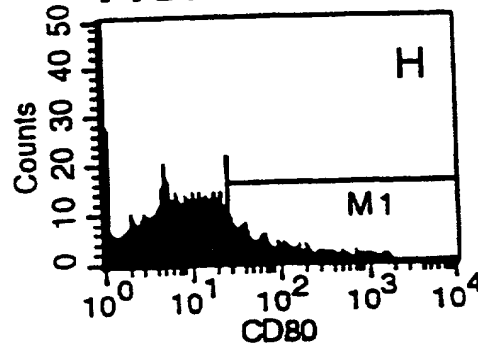
FIG. 4G



% Pos MFI

61 74

FIG. 4H



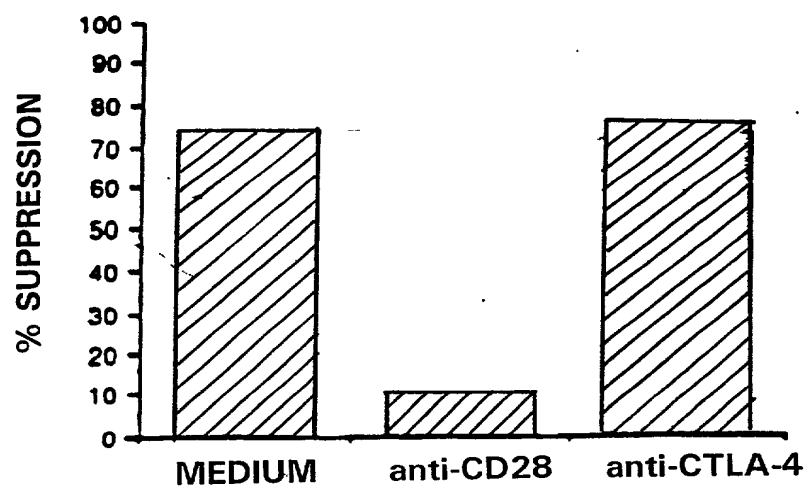
% Pos MFI

17 110

007221" TE 94/60

7/73

FIG. 5



8/73

FIG. 6A

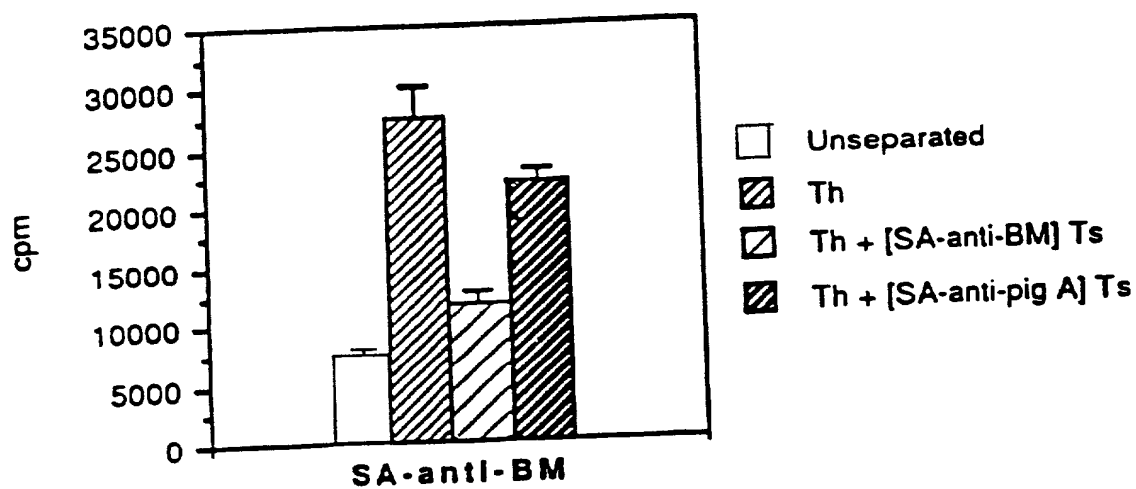
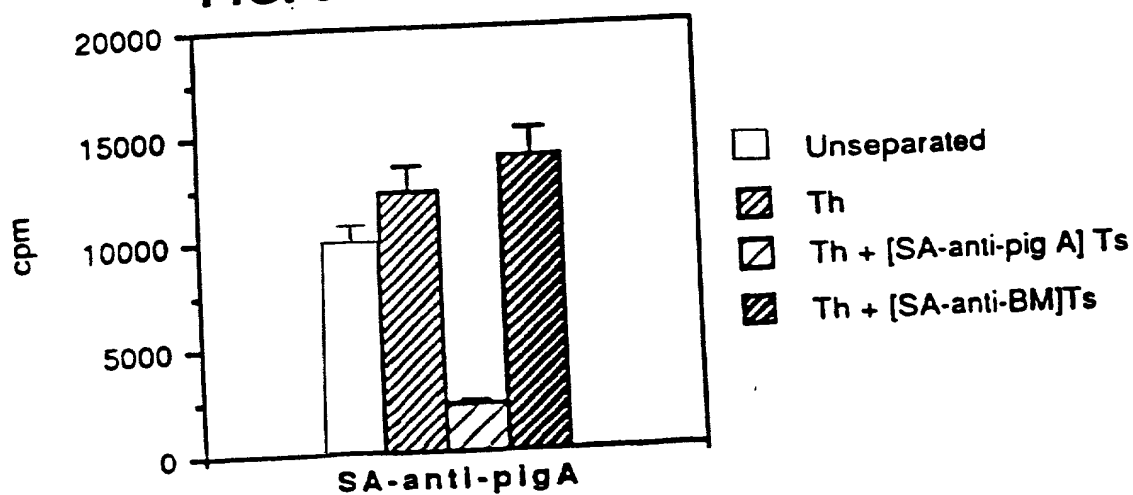


FIG. 6B



9/73

FIG. 7A

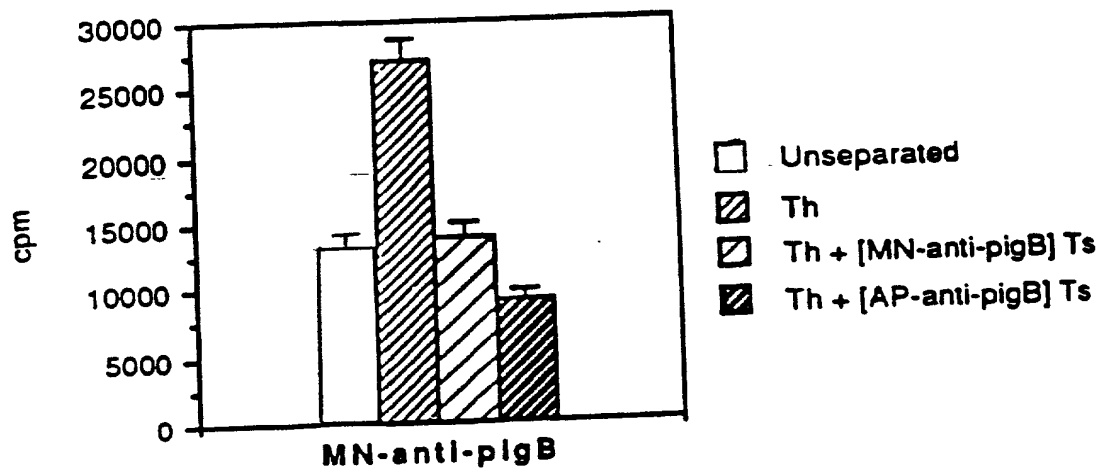
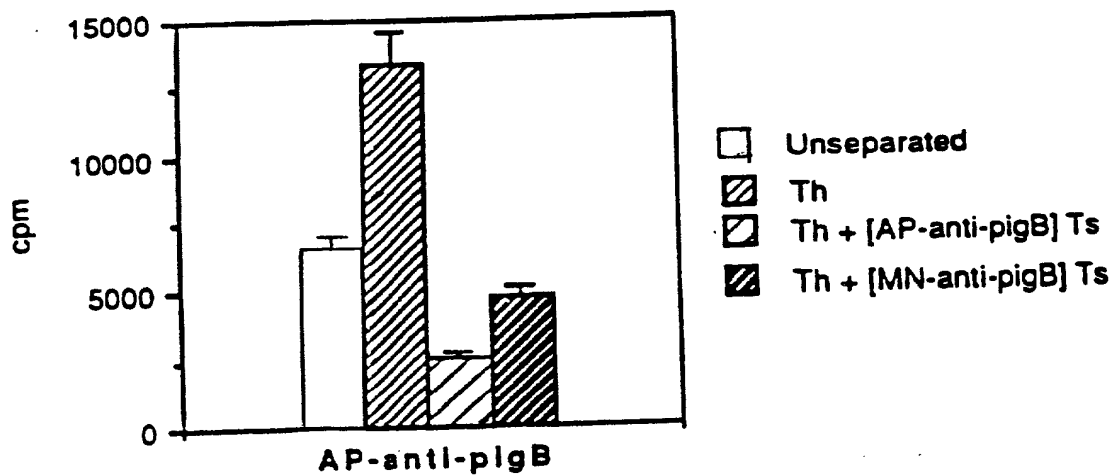


FIG. 7B



10/73

FIG. 8A

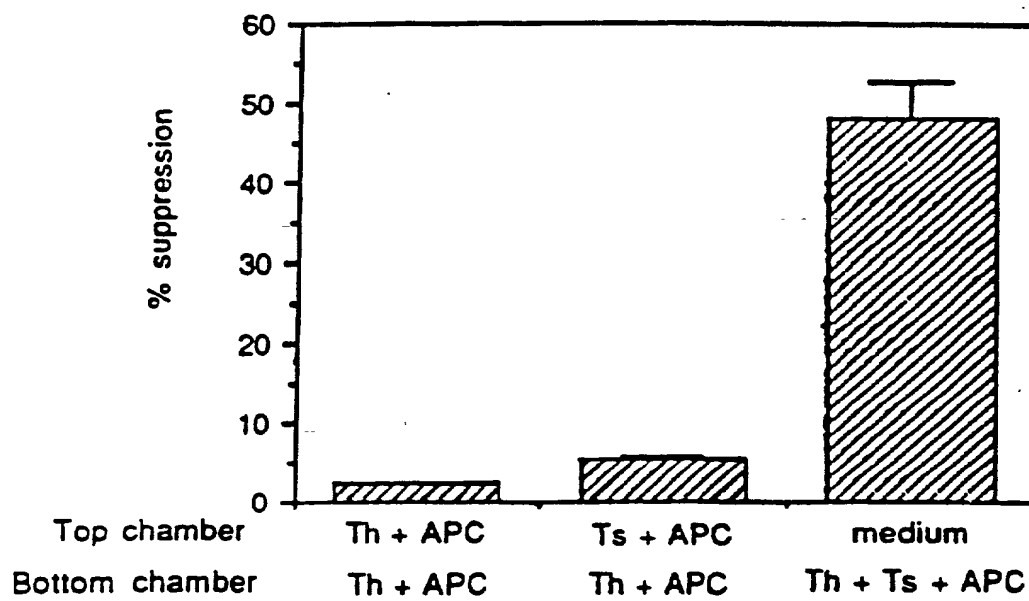
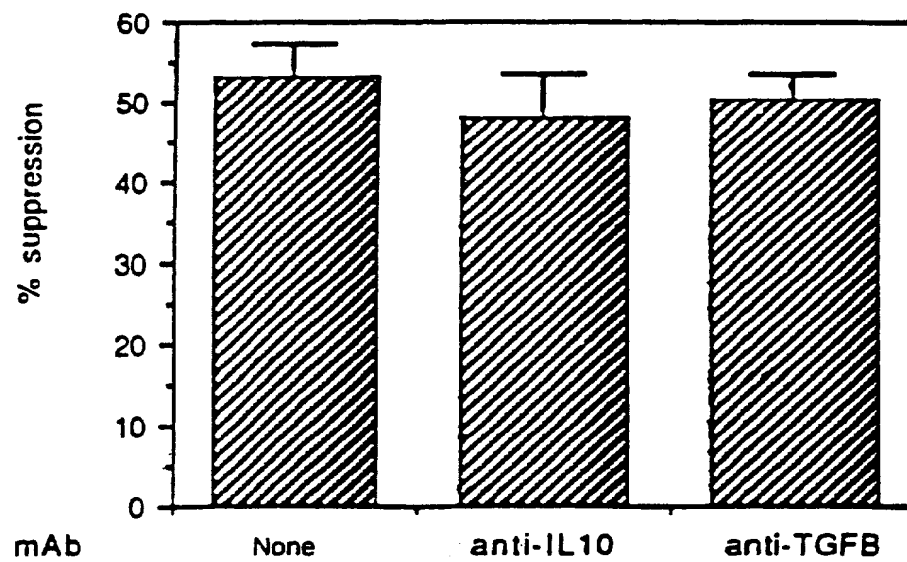


FIG. 8B



11/73

T helper cells

FIG. 9A

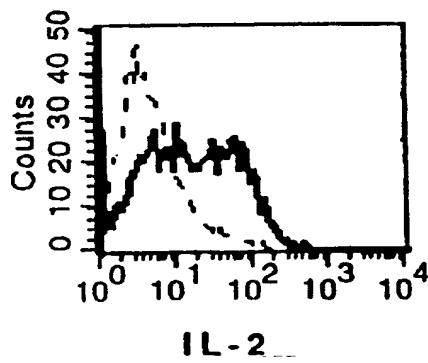


FIG. 9B

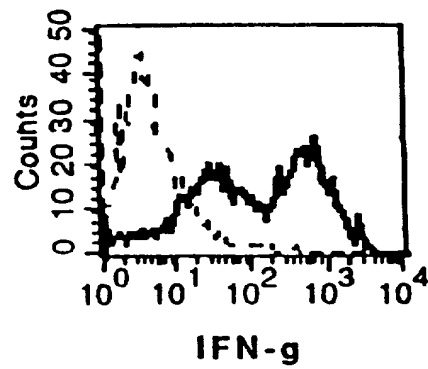


FIG. 9C

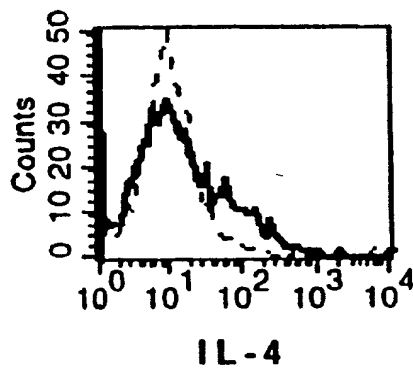
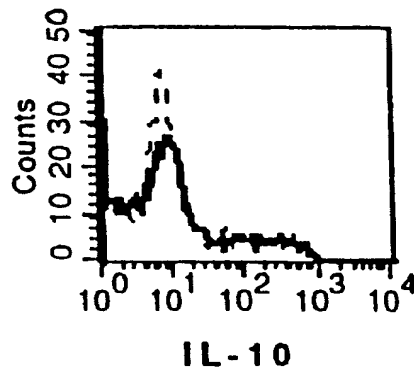
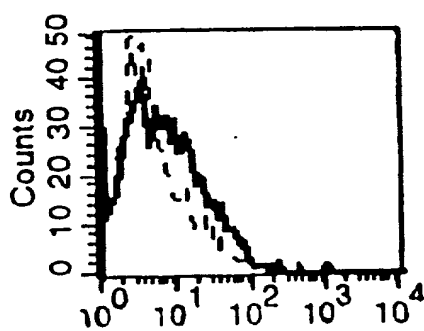


FIG. 9D



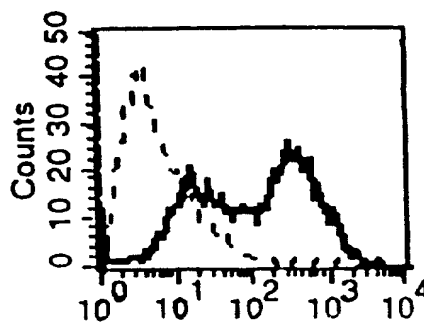
12/73

T suppressor cells



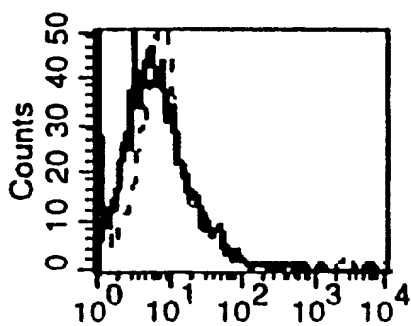
IL-2

FIG. 9E



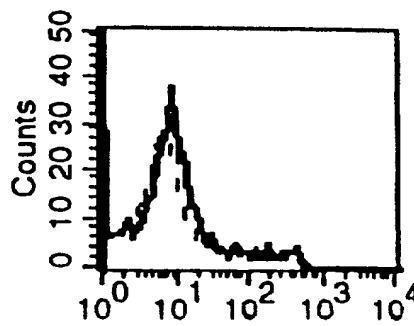
IFN-g

FIG. 9F



IL-4

FIG. 9G



IL-10

FIG. 9H

007227-TE-9H-260

FIG. 10A

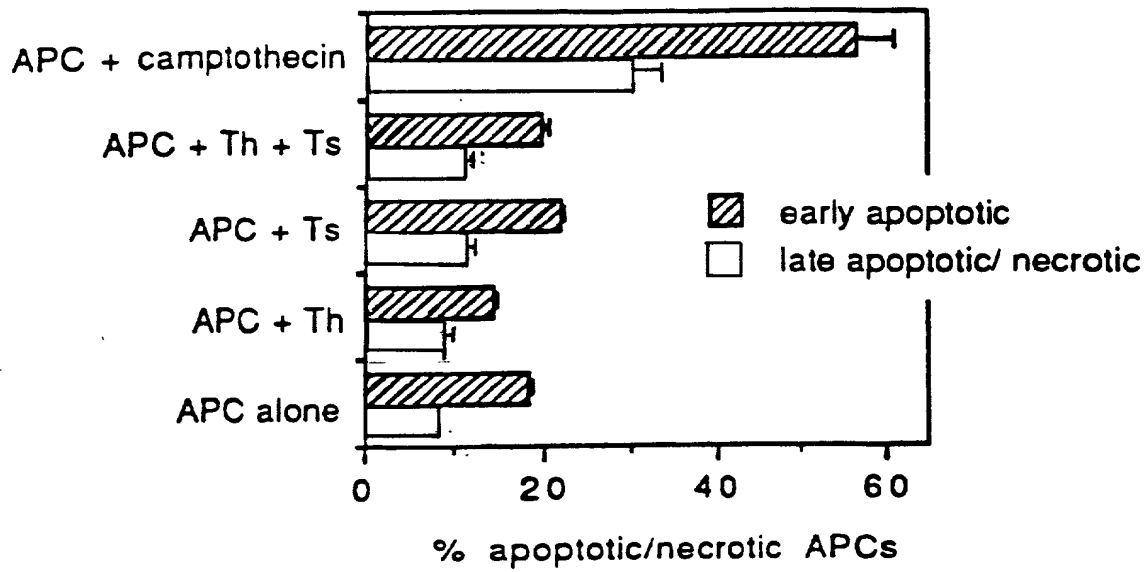
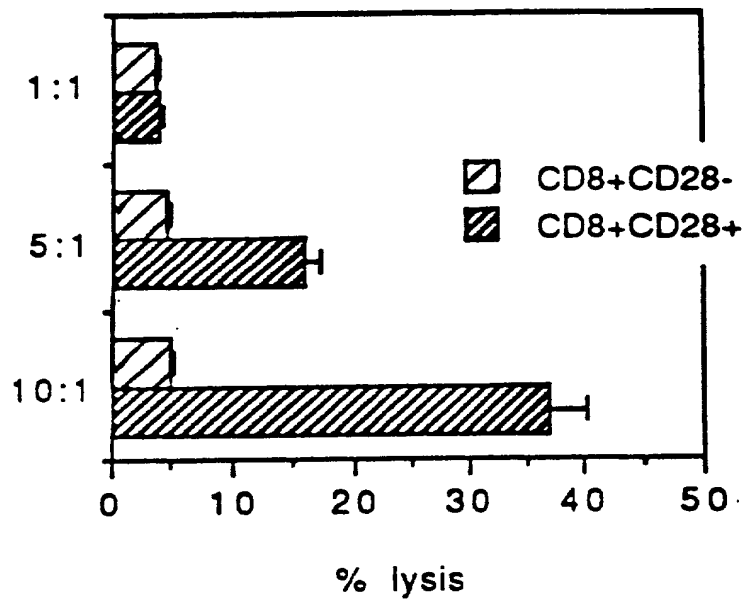


FIG. 10B

Effector/
Target

14/73

FIG. 10C

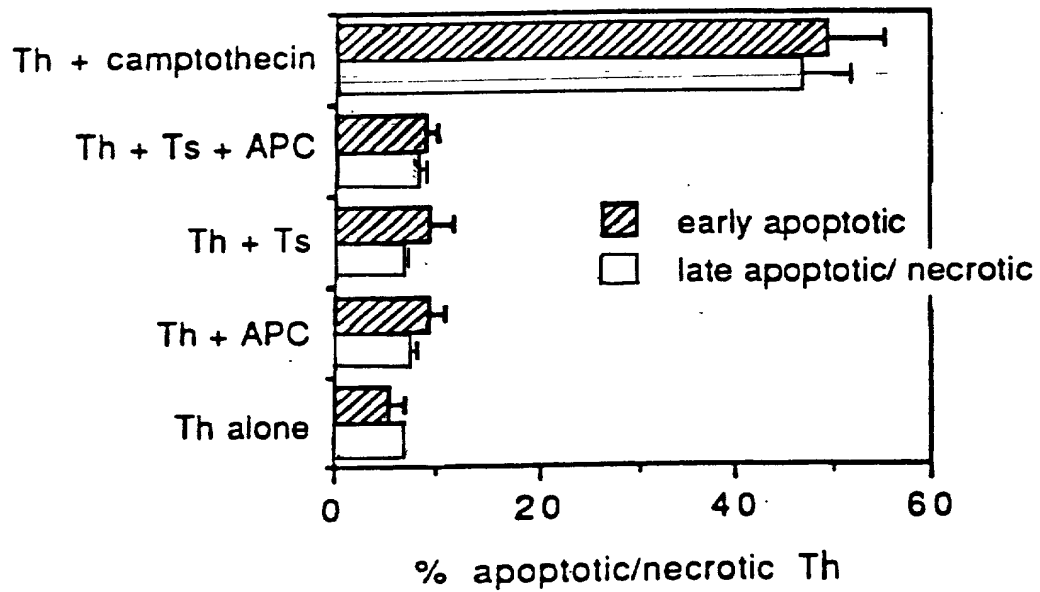


FIG. 11A

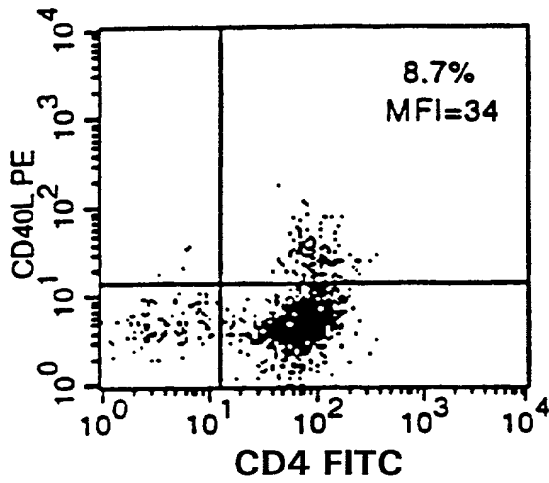


FIG. 11B

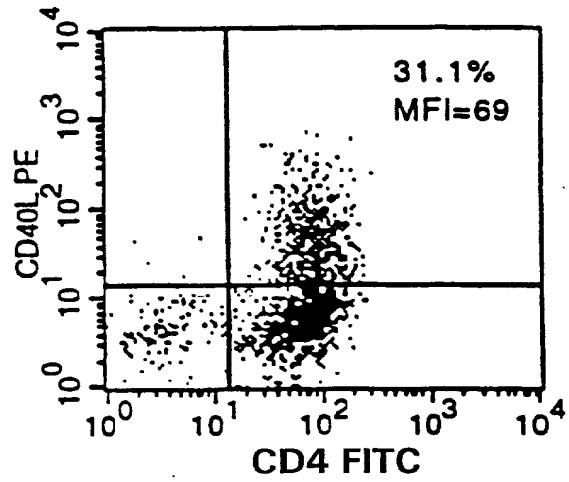


FIG. 11C

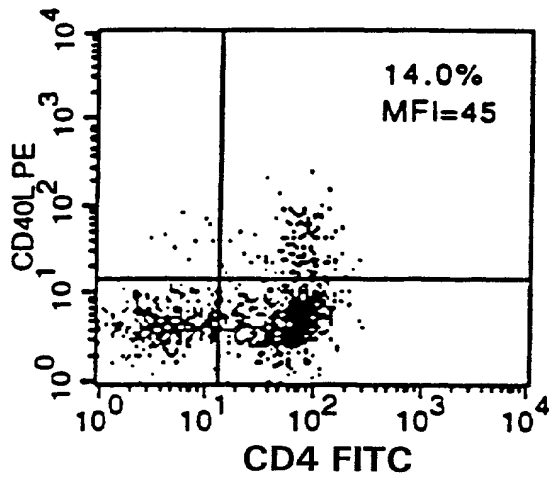
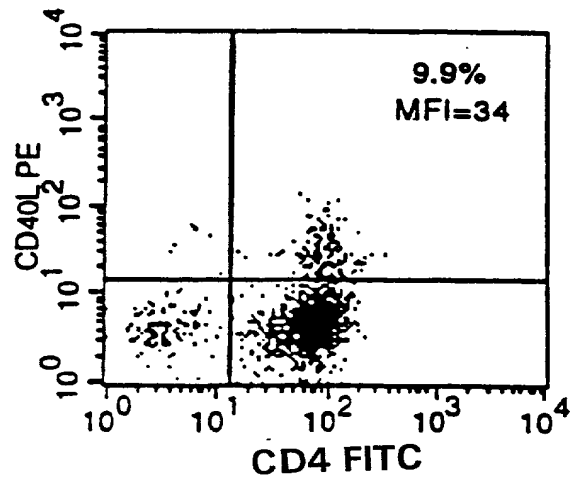
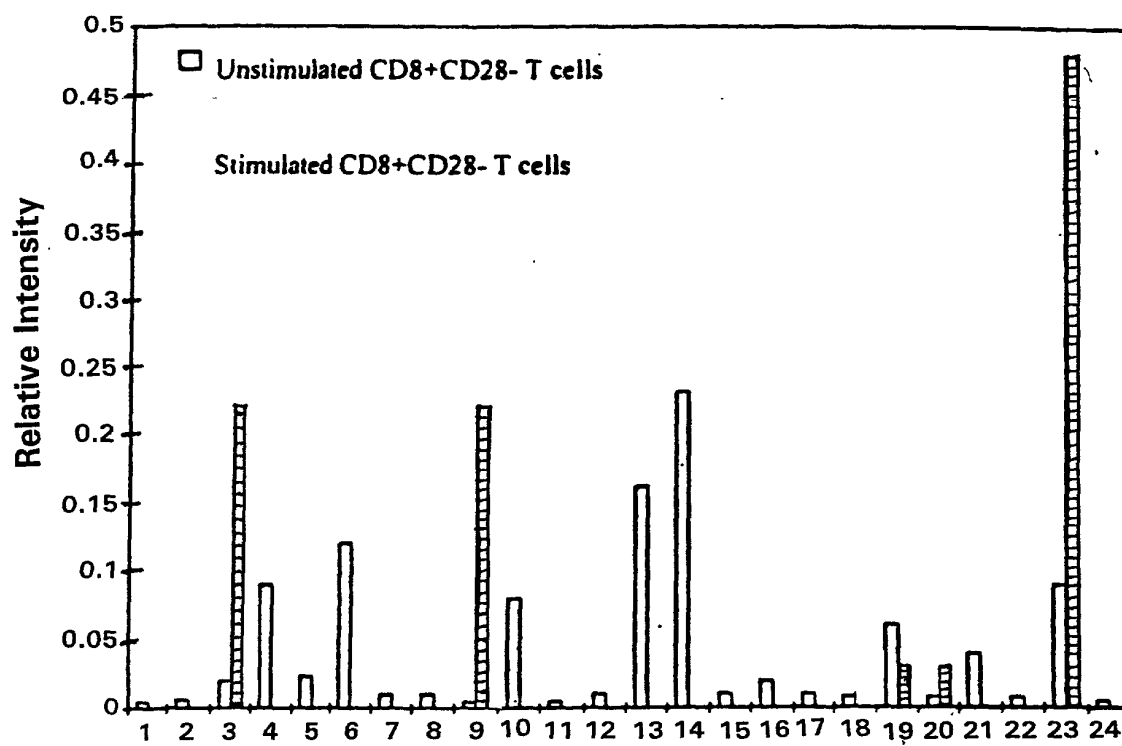


FIG. 11D



V beta families



17/73

FIG. 13A

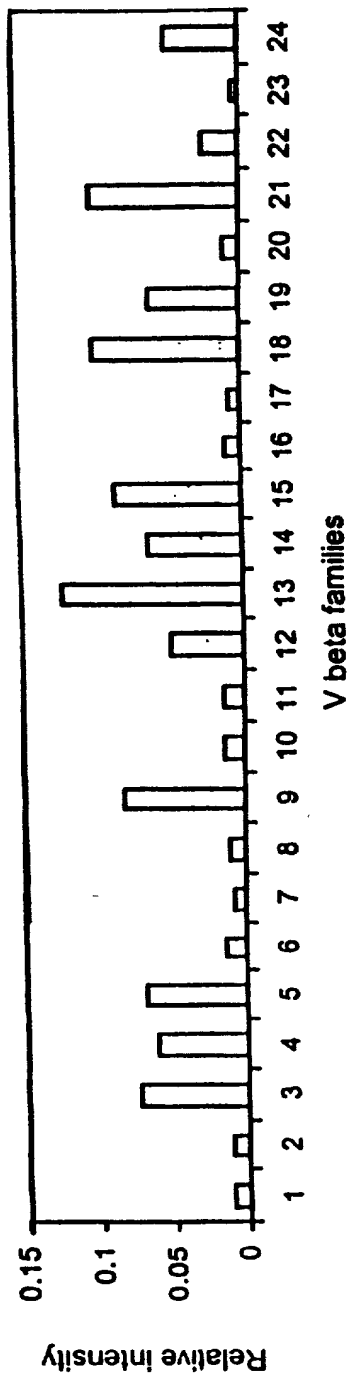


FIG. 13B

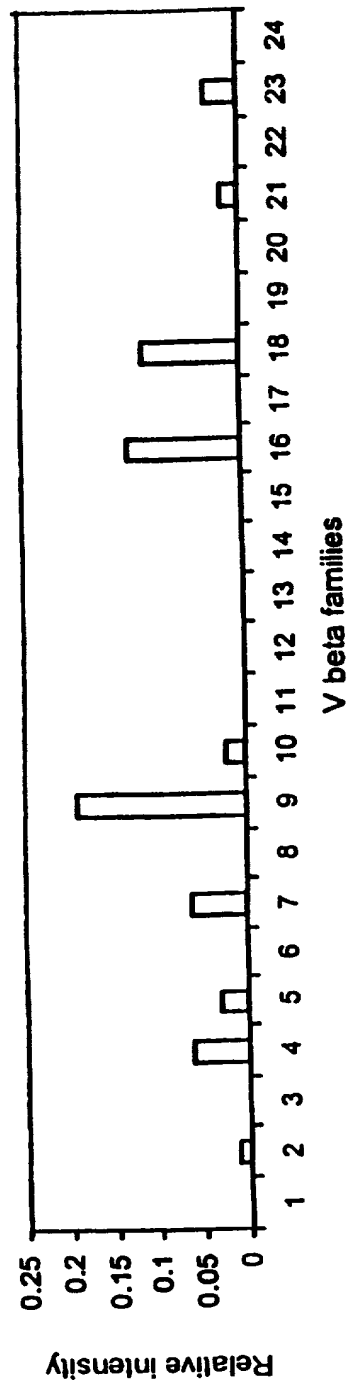


FIG. 13C

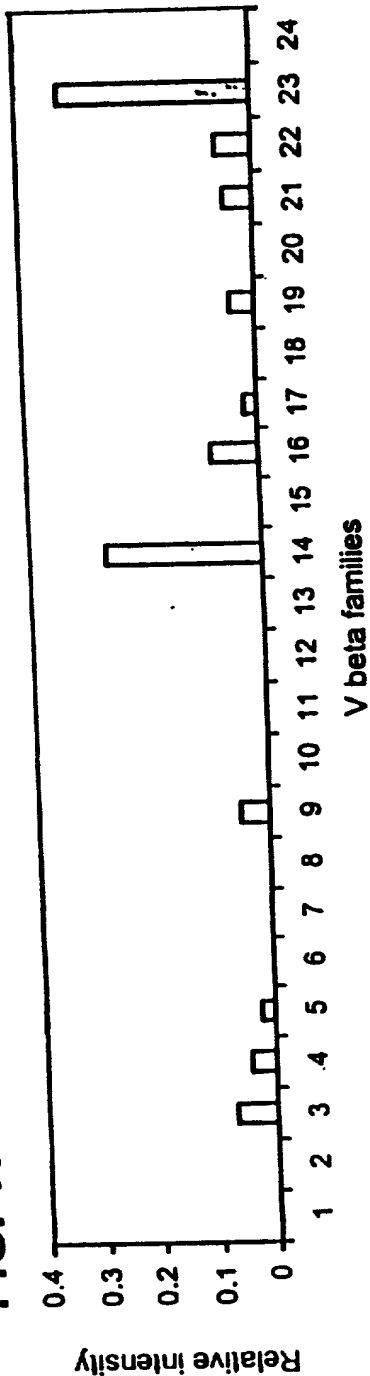
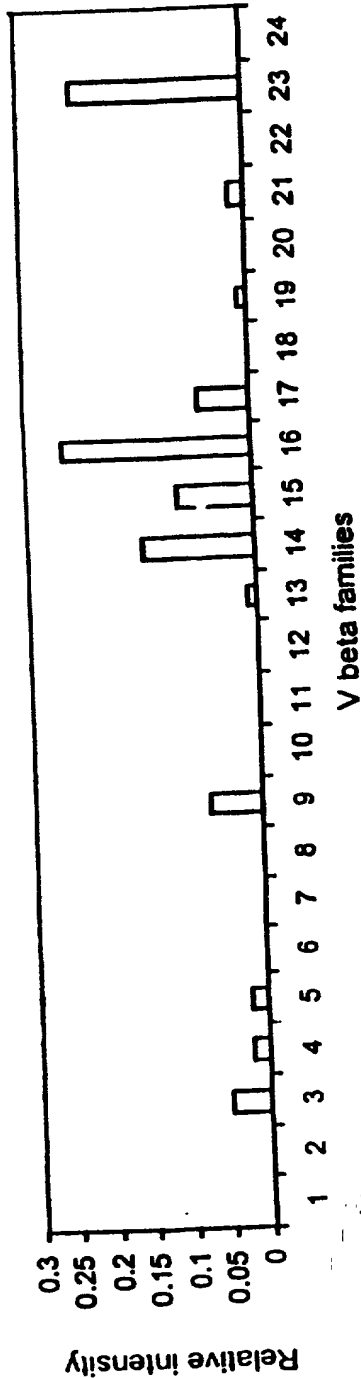


FIG. 13D



19/73

FIG. 14A

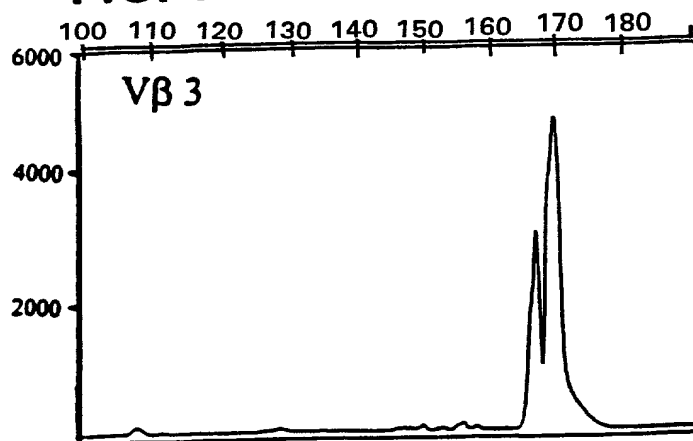


FIG. 14B

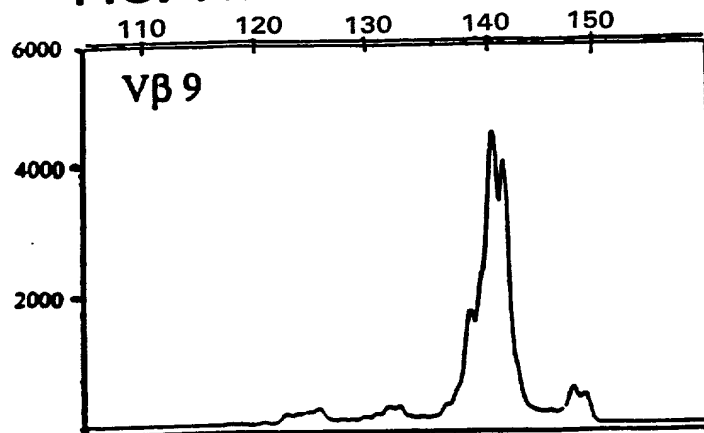
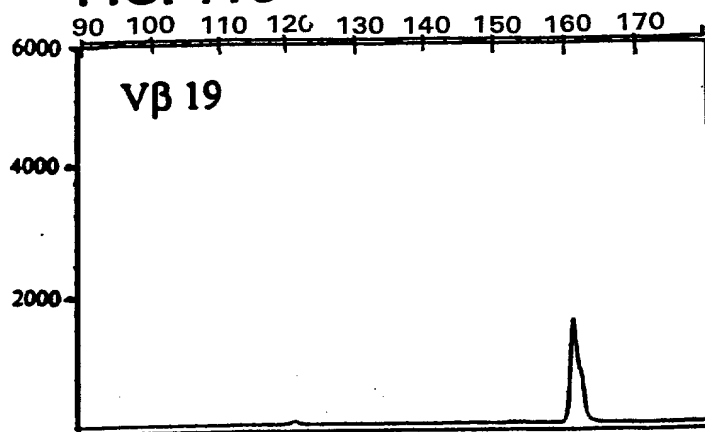


FIG. 14C

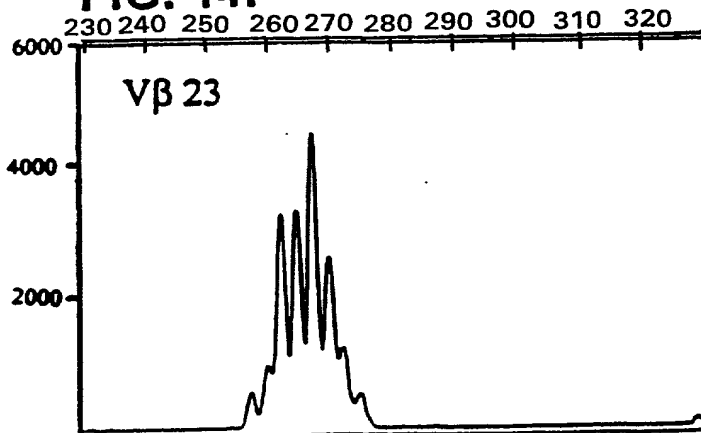
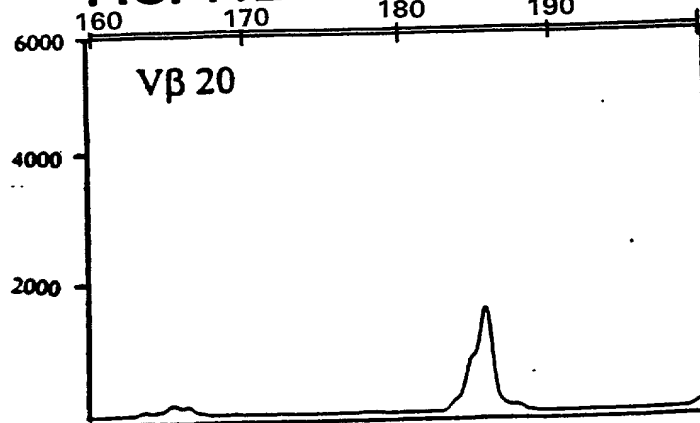
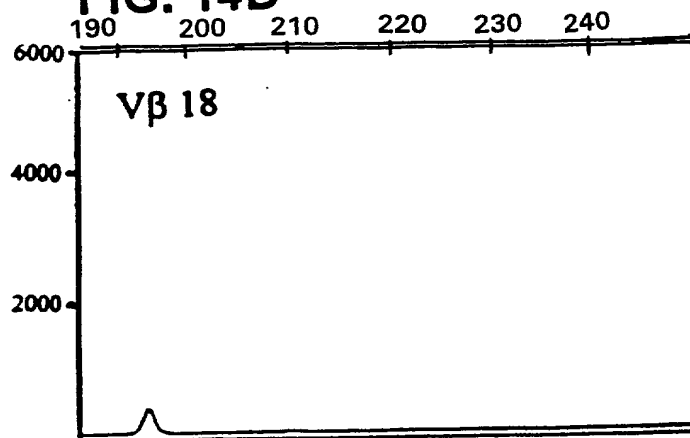


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Figure 1 consists of 12 bar charts, labeled (a) through (l), each representing a different demographic or attitudinal variable. The y-axis for all charts is 'Percentage of respondents' ranging from 0 to 100. The x-axis for each chart has two categories: 'Clinton' and 'Bush'. The data for each chart is as follows:

- (a) Age: Clinton (18-24: 10%, 25-34: 15%, 35-44: 20%, 45-54: 25%, 55-64: 20%, 65+: 10%), Bush (18-24: 5%, 25-34: 10%, 35-44: 15%, 45-54: 20%, 55-64: 25%, 65+: 25%).
- (b) Sex: Clinton (Male: 55%, Female: 45%), Bush (Male: 50%, Female: 50%).
- (c) Education: Clinton (High school or less: 30%, Some college: 35%, Bachelor's: 30%, Graduate: 5%), Bush (High school or less: 35%, Some college: 30%, Bachelor's: 25%, Graduate: 10%).
- (d) Income: Clinton (<\$10,000: 15%, \$10,000-\$19,999: 20%, \$20,000-\$29,999: 25%, \$30,000-\$39,999: 20%, \$40,000-\$49,999: 15%, \$50,000+: 5%), Bush (<\$10,000: 10%, \$10,000-\$19,999: 15%, \$20,000-\$29,999: 20%, \$30,000-\$39,999: 25%, \$40,000-\$49,999: 20%, \$50,000+: 10%).
- (e) Employment: Clinton (Not employed: 10%, Part-time: 15%, Full-time: 75%), Bush (Not employed: 15%, Part-time: 20%, Full-time: 65%).
- (f) Home ownership: Clinton (Own: 85%, Rent: 15%), Bush (Own: 80%, Rent: 20%).
- (g) Marital status: Clinton (Married: 65%, Single: 25%, Divorced: 5%, Widowed: 5%), Bush (Married: 60%, Single: 30%, Divorced: 5%, Widowed: 5%).
- (h) Political affiliation: Clinton (Democrat: 85%, Republican: 10%, Independent: 5%), Bush (Democrat: 75%, Republican: 20%, Independent: 5%).
- (i) Party identification: Clinton (Democrat: 85%, Republican: 10%, Independent: 5%), Bush (Democrat: 75%, Republican: 20%, Independent: 5%).
- (j) Trust in Clinton: Clinton (No trust: 10%, Little trust: 20%, Some trust: 30%, A lot of trust: 40%), Bush (No trust: 15%, Little trust: 25%, Some trust: 30%, A lot of trust: 30%).
- (k) Trust in Bush: Clinton (No trust: 15%, Little trust: 25%, Some trust: 30%, A lot of trust: 30%), Bush (No trust: 10%, Little trust: 20%, Some trust: 30%, A lot of trust: 40%).
- (l) Confidence in Clinton: Clinton (No confidence: 10%, Little confidence: 20%, Some confidence: 30%, A lot of confidence: 40%), Bush (No confidence: 15%, Little confidence: 25%, Some confidence: 30%, A lot of confidence: 30%).

IR spectrum of compound 18. The x-axis represents wavenumber in cm⁻¹, ranging from 190 to 240. The y-axis represents intensity, ranging from 0 to 6000. A sharp peak is observed at approximately 1900 cm⁻¹, labeled $v\beta$ 18.



21/73

FIG. 15A

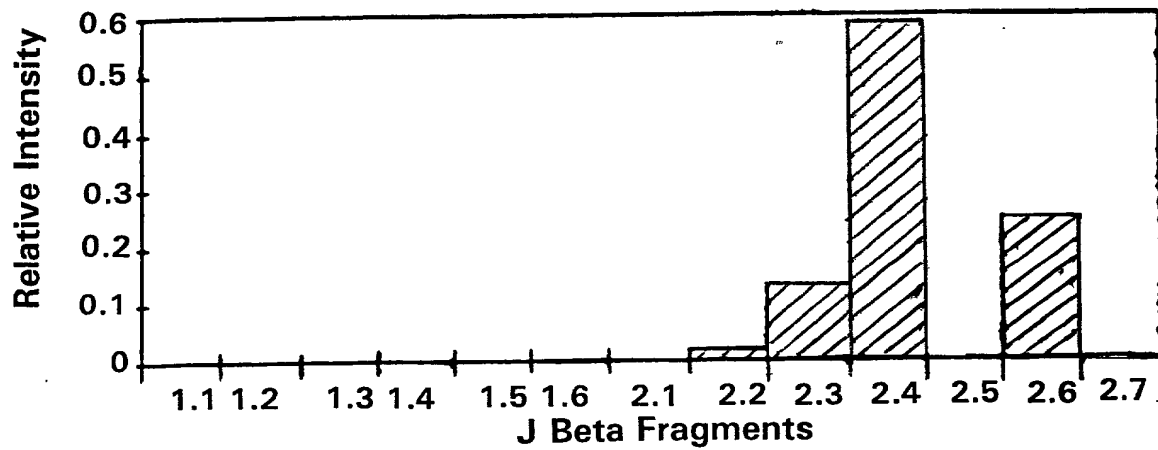


FIG. 15B

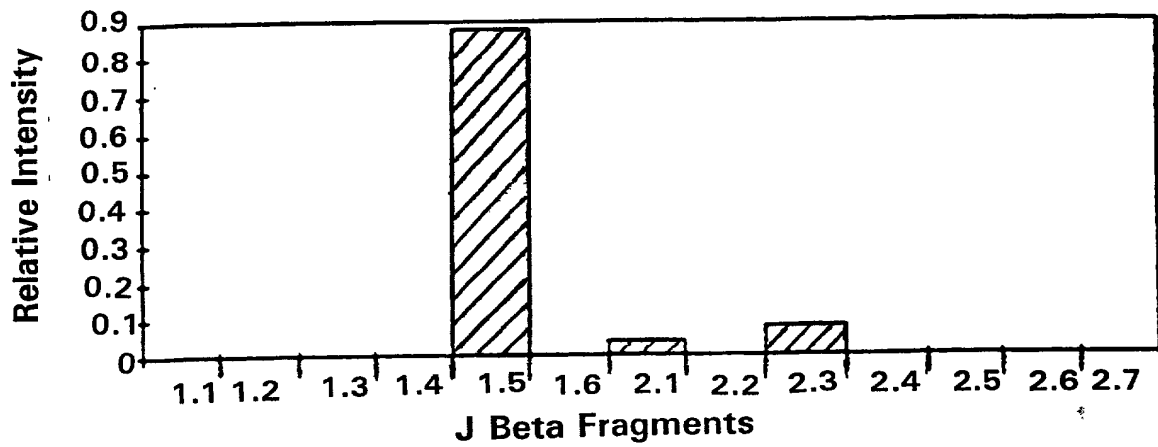
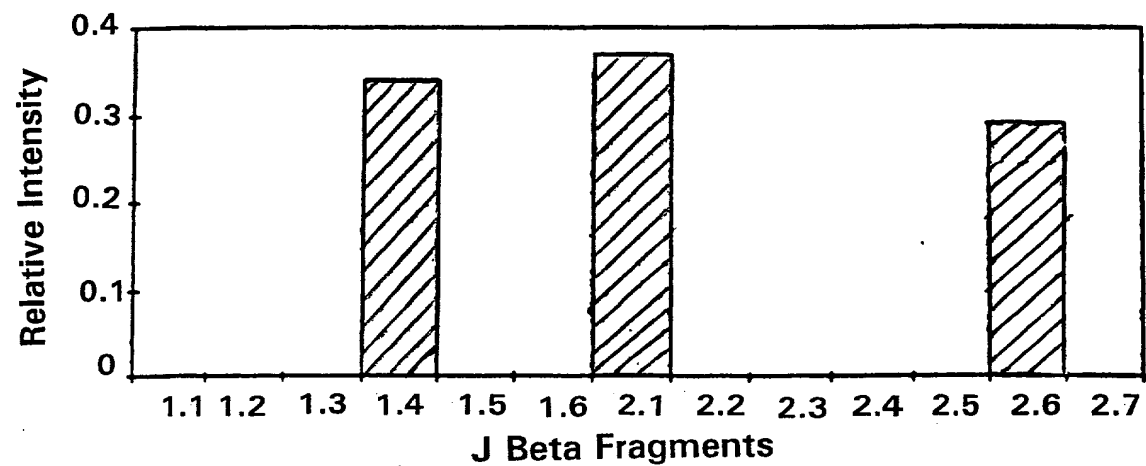
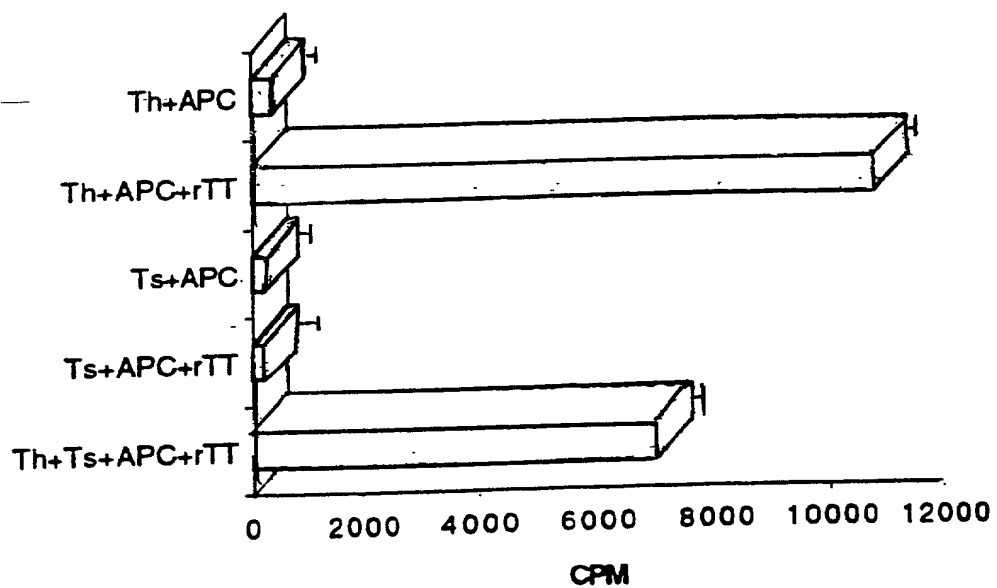


FIG. 15C



22/73

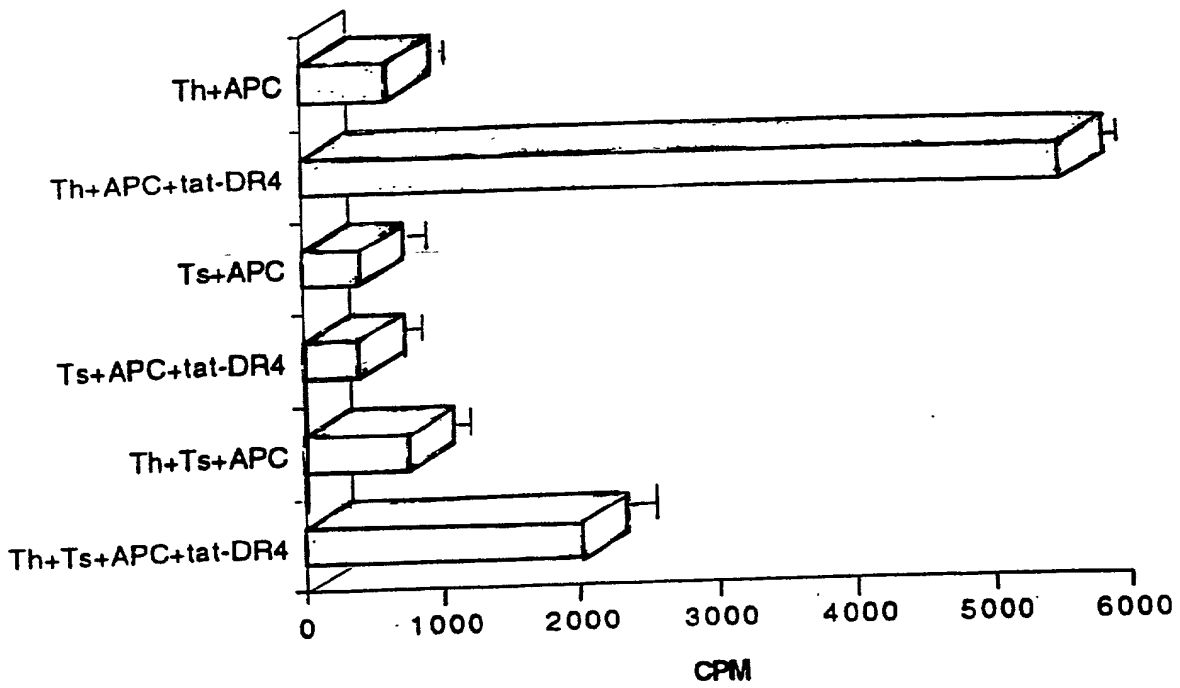
FIG. 16



094634-122100

23/73

FIG. 17



0074634-1400

FIG. 18A

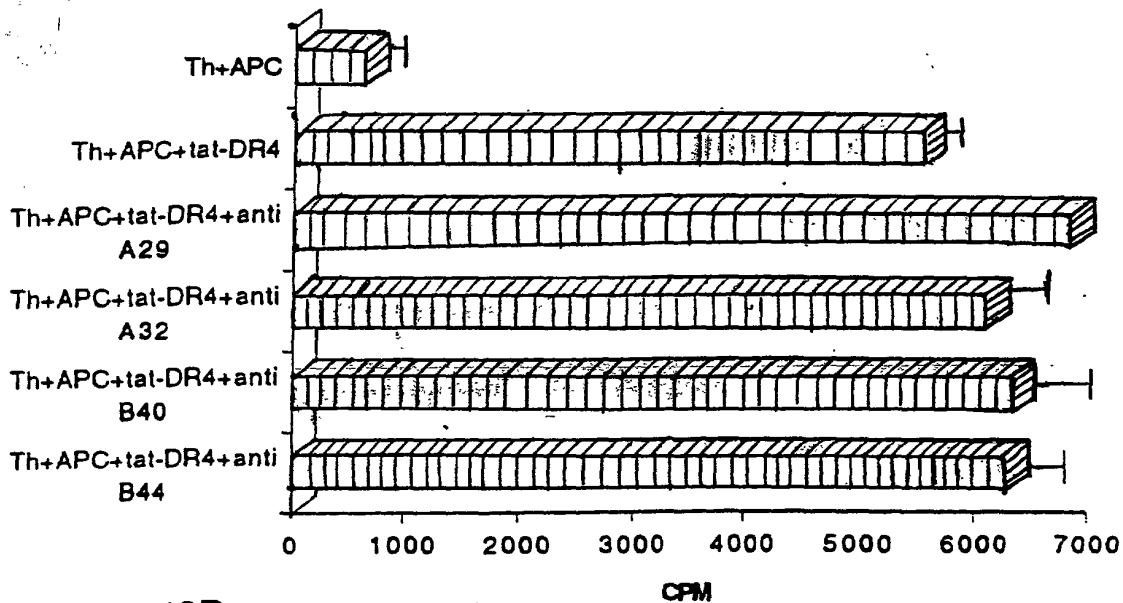
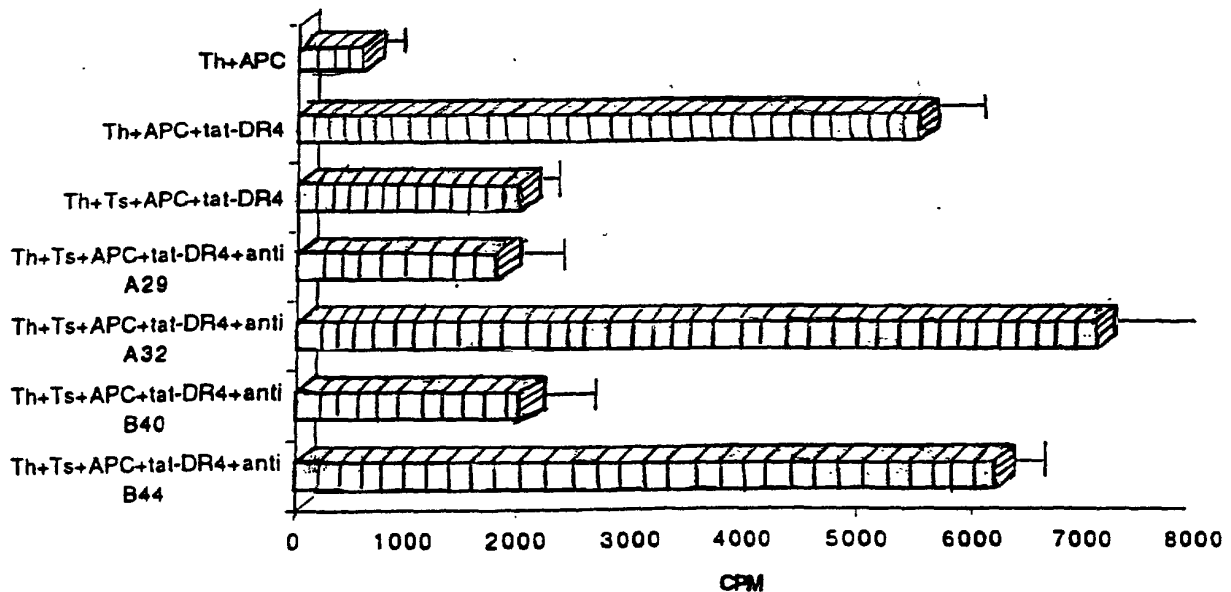


FIG. 18B



25/73

FIG. 19A-1

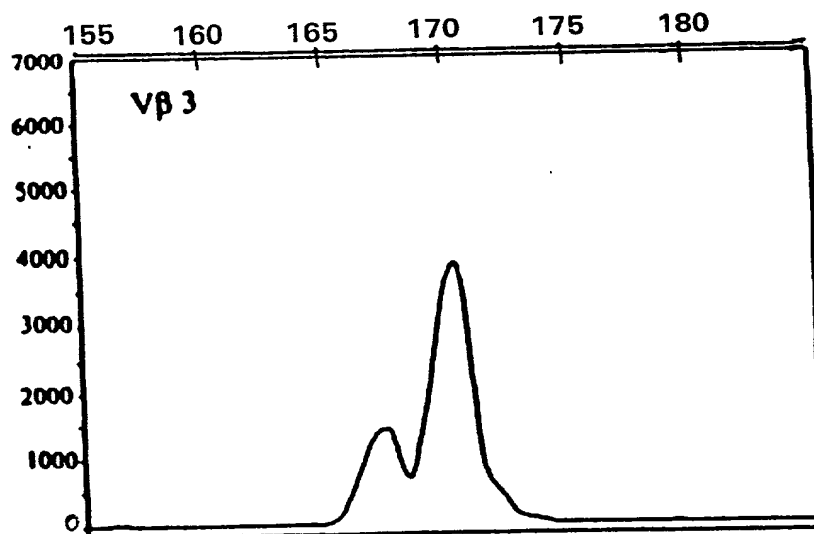


FIG. 19A-2

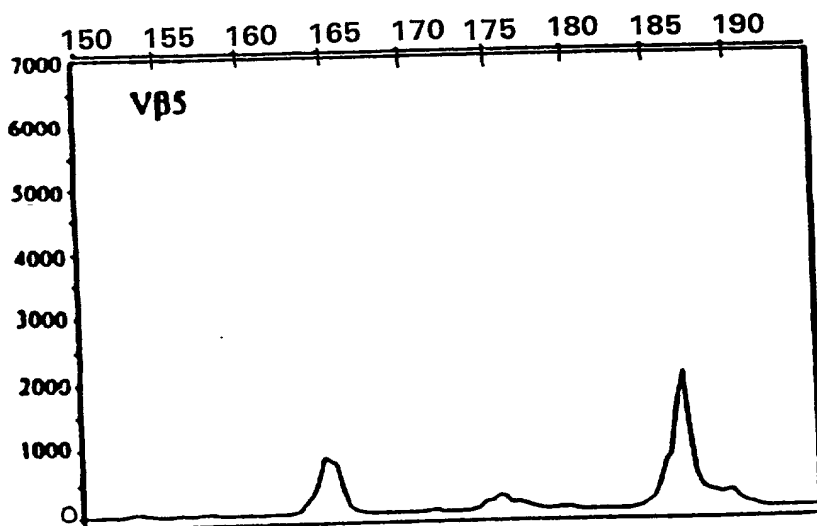
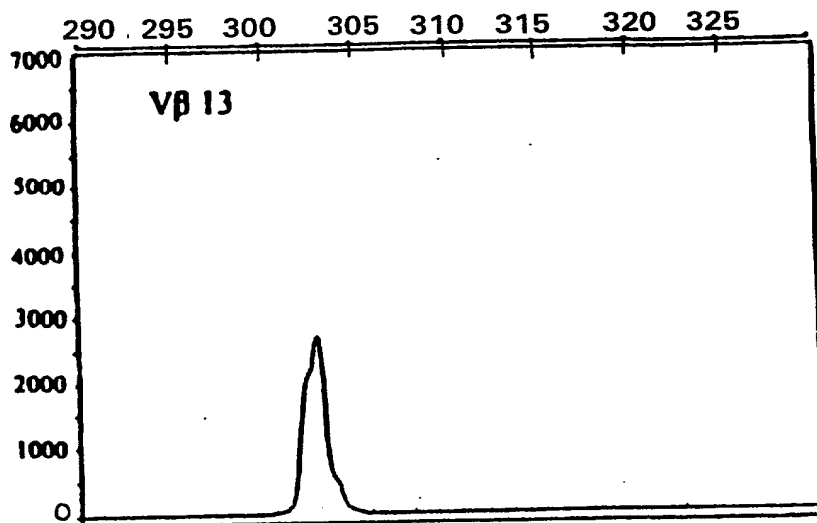


FIG. 19A-3



26/73

FIG. 19A-4

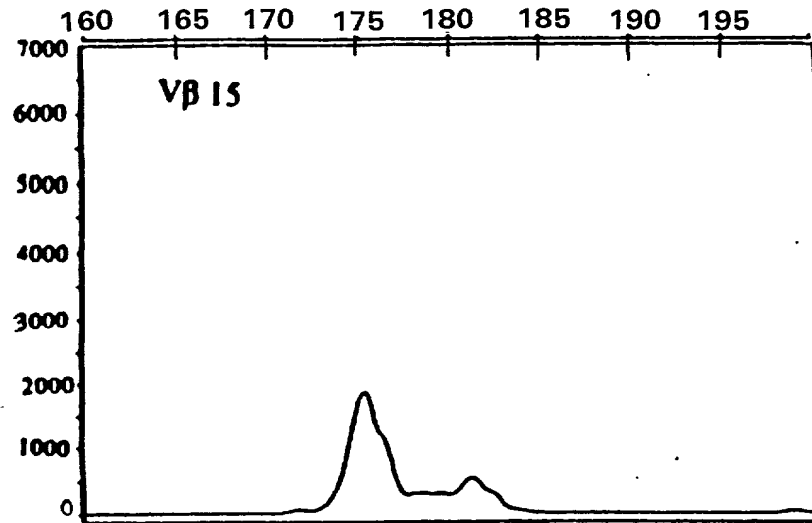
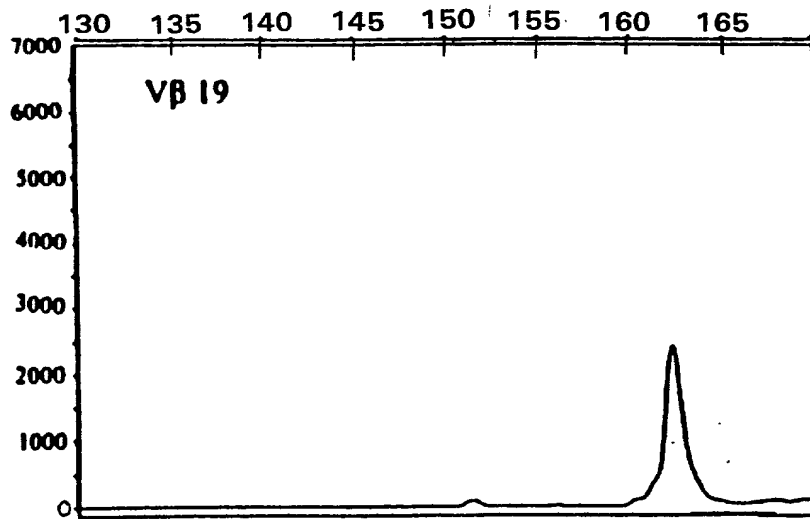


FIG. 19A-5



27/73

FIG. 19B-1

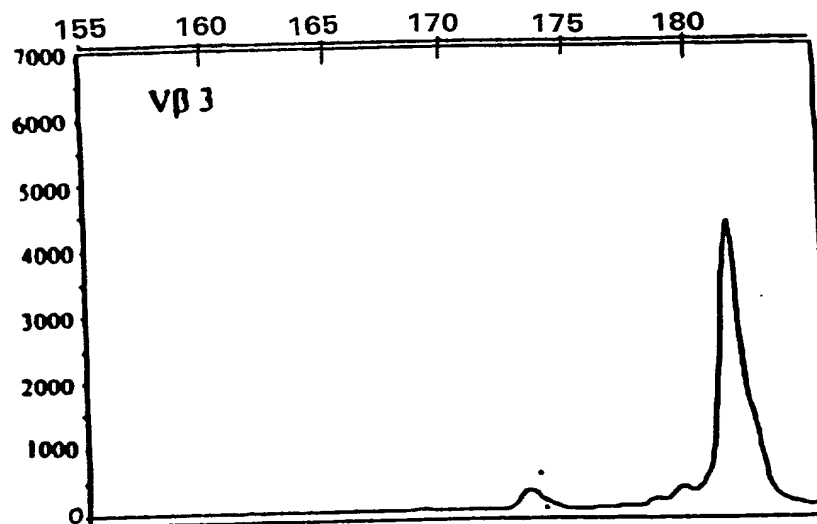


FIG. 19B-2

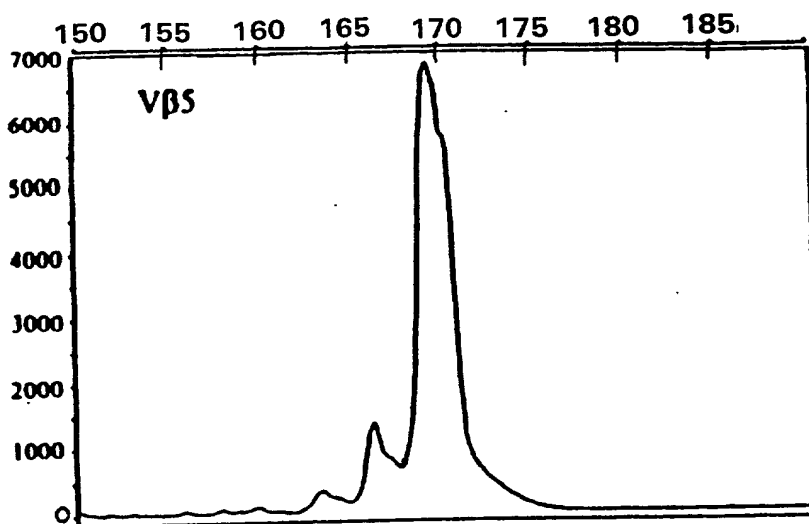
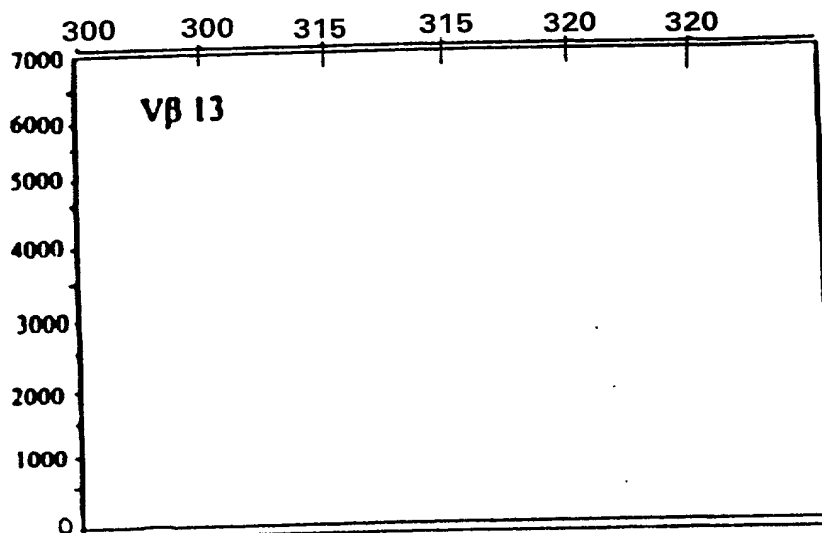


FIG. 19B-3



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28/73

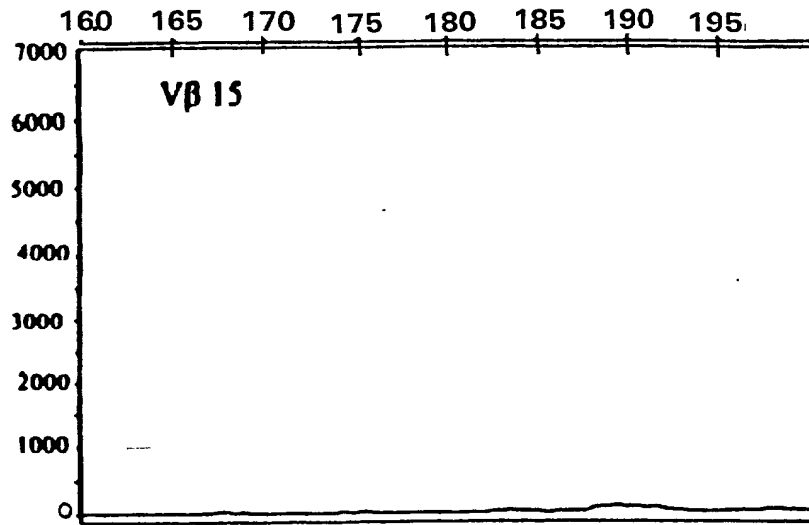


FIG. 19B-4

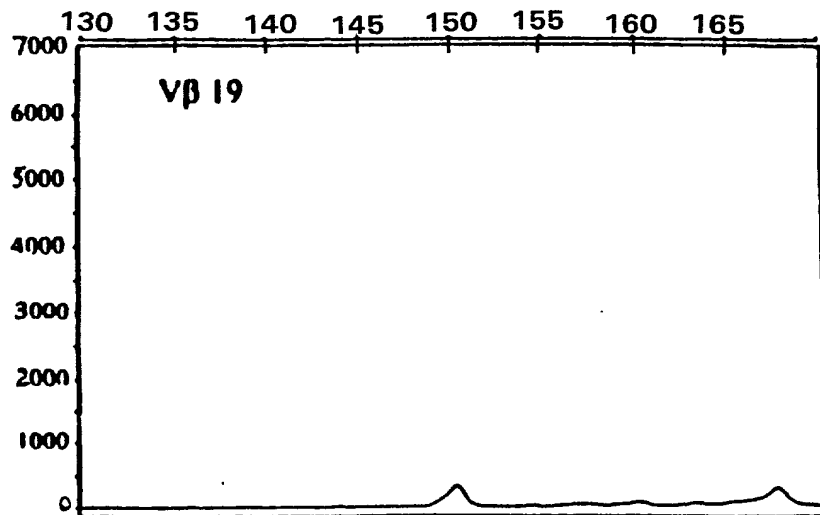


FIG. 19B-5

29/73

FIG. 19C-1

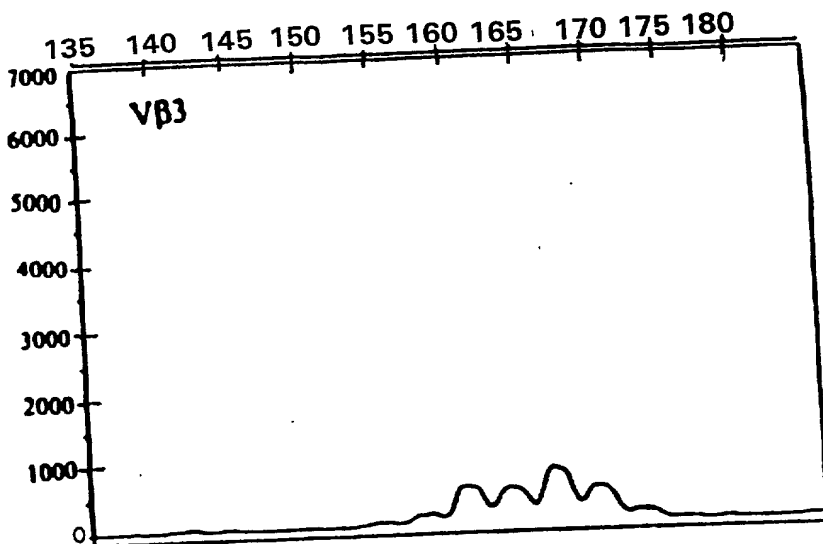


FIG. 19C-2

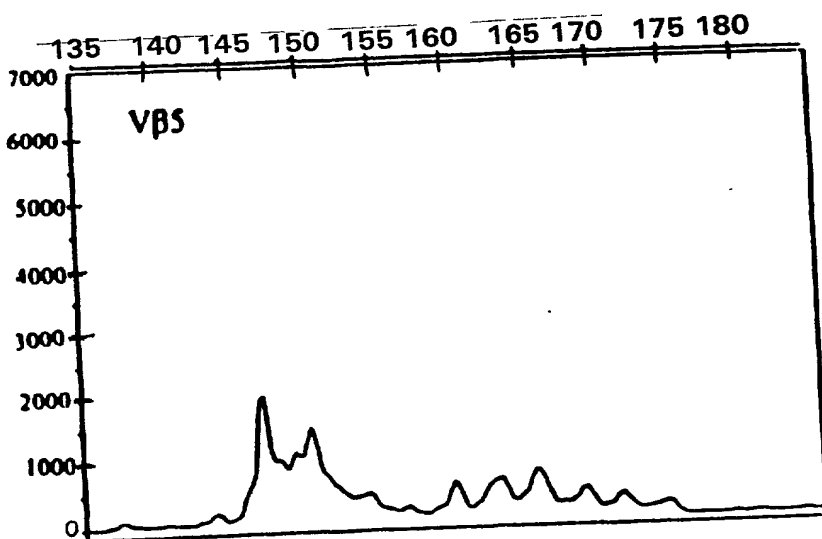
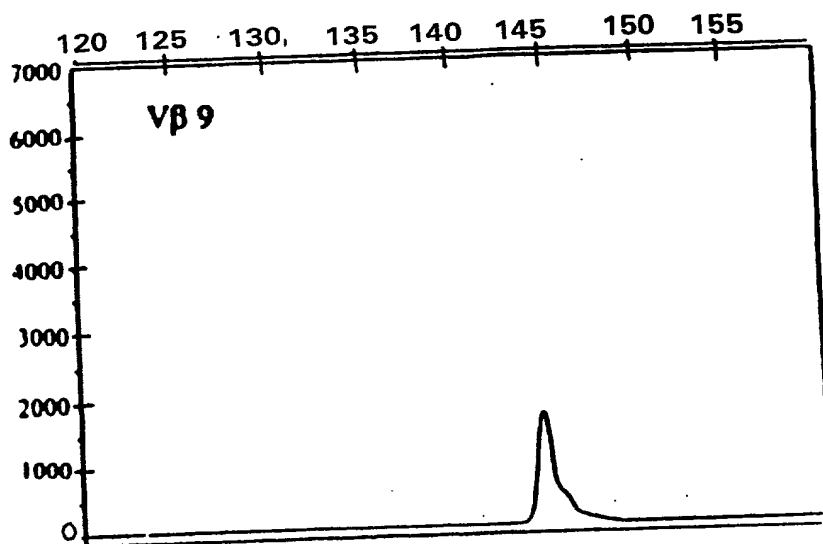


FIG. 19C-3



30/73

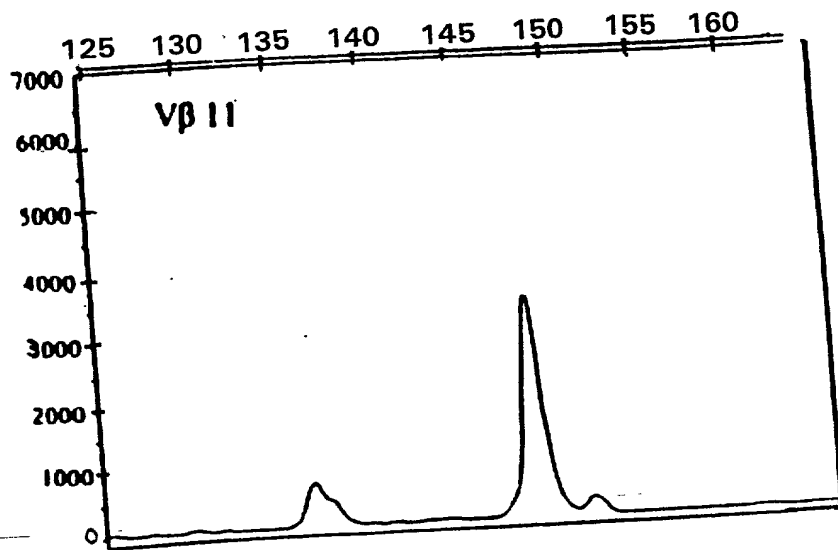


FIG. 19C-4

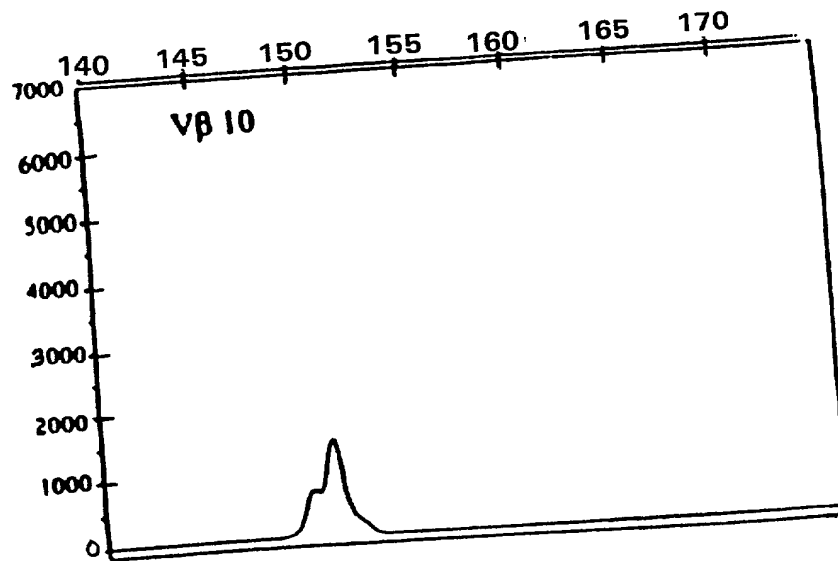


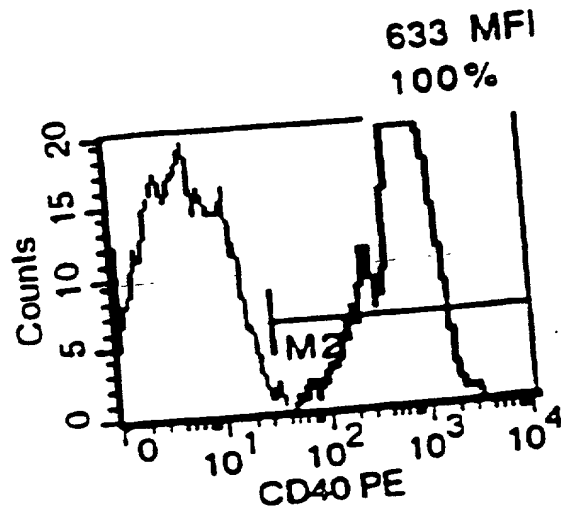
FIG. 19C-5

00745311 123100

31/73

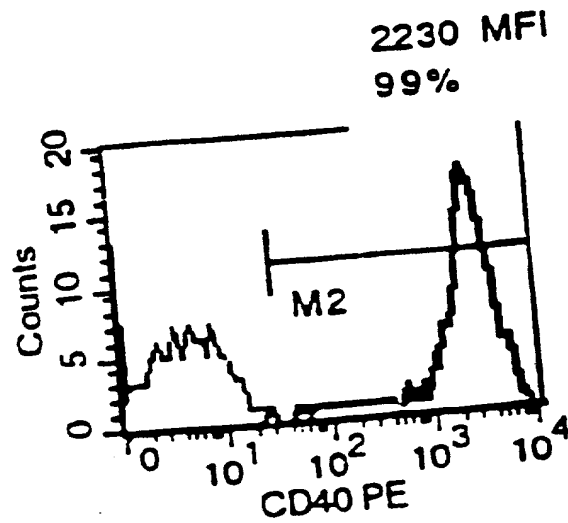
FIG. 20A

CD40



APC+tat-DR4

FIG. 20B

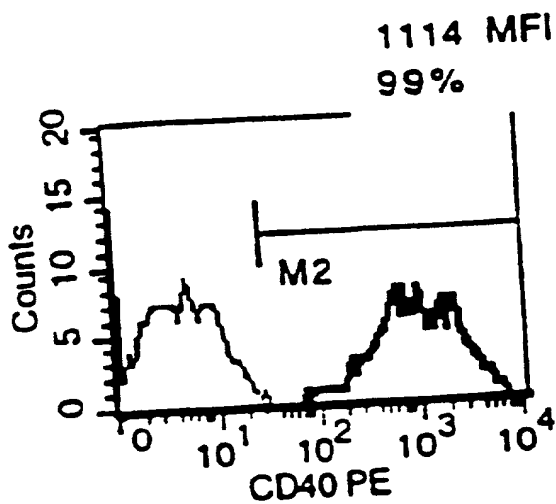


Th+APC+tat-DR4

32/73

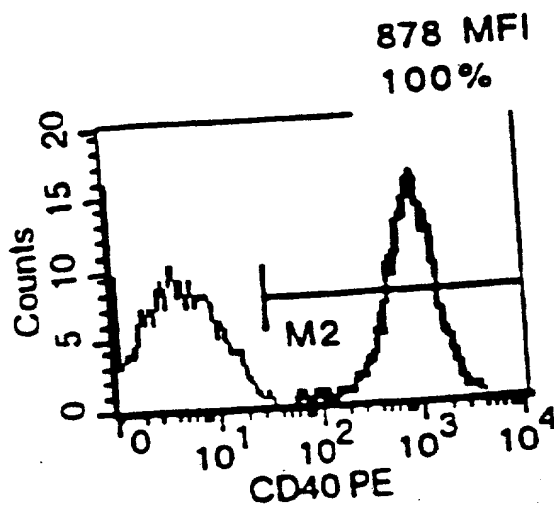
CD40

FIG. 20C



Th+Ts+APC+tat-DR4

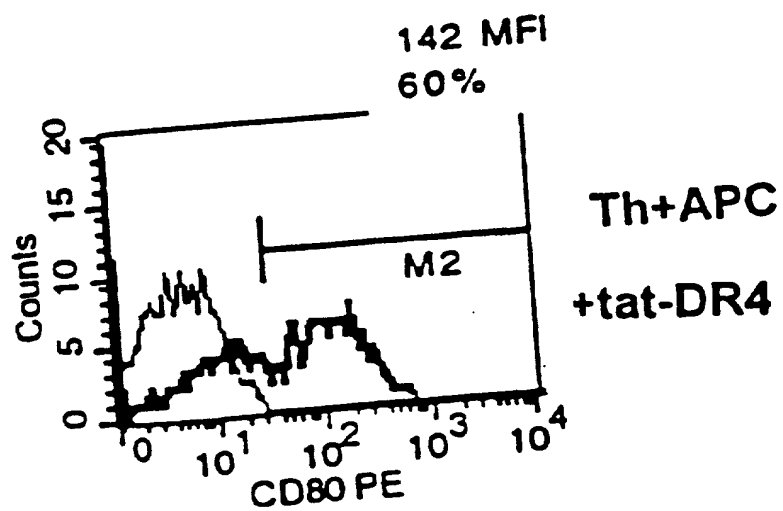
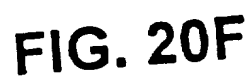
FIG. 20D



Ts+APC+tat-DR4

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FIG. 20E



34/73

CD80

FIG. 20G

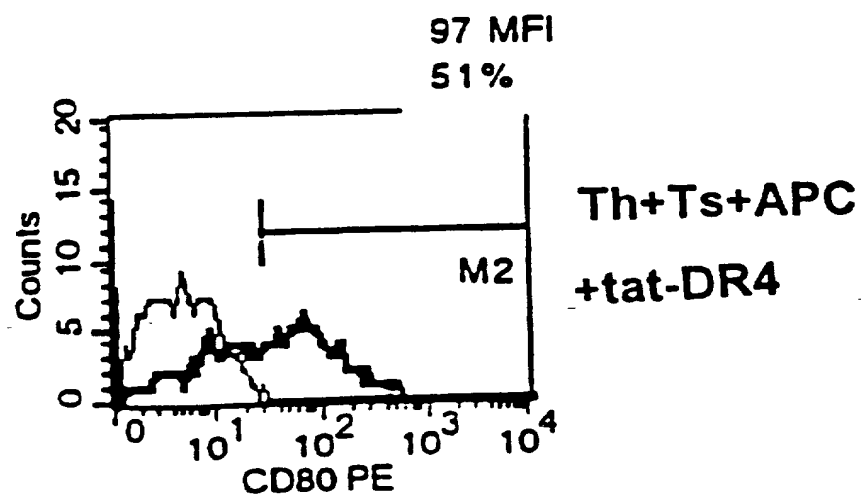
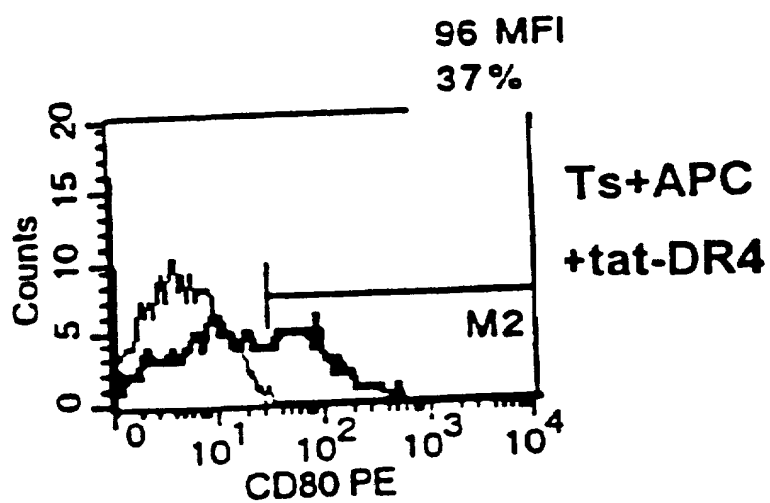
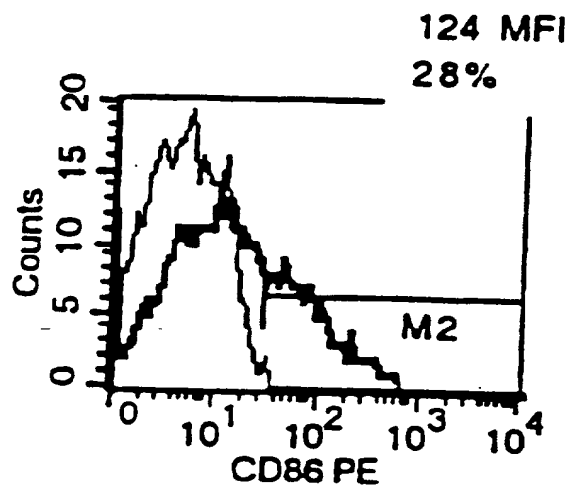


FIG. 20H



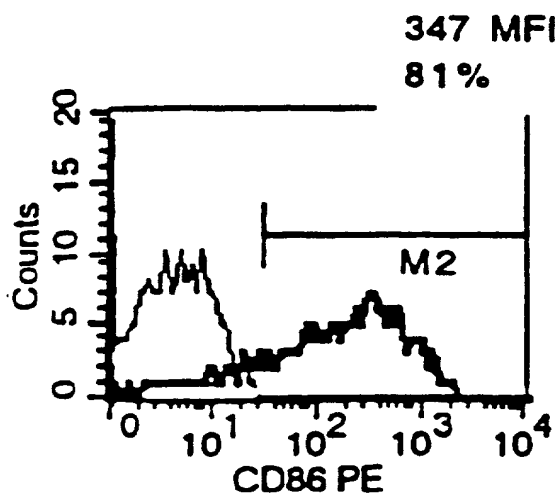
35/73

CD86



APC+tat-DR4

FIG. 20I



Th+APC+tat-DR4

FIG. 20J

007221" TEE94/60

36/73

CD86

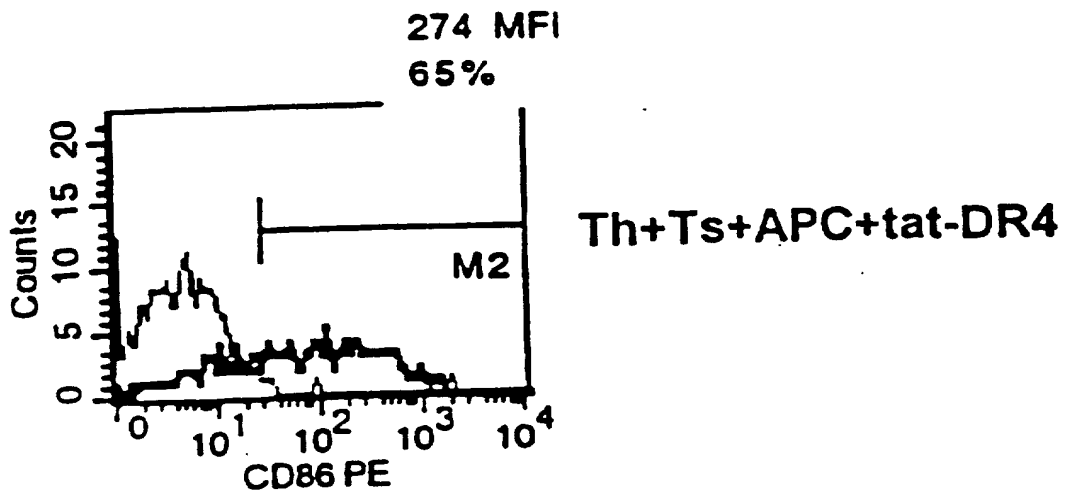


FIG. 20K

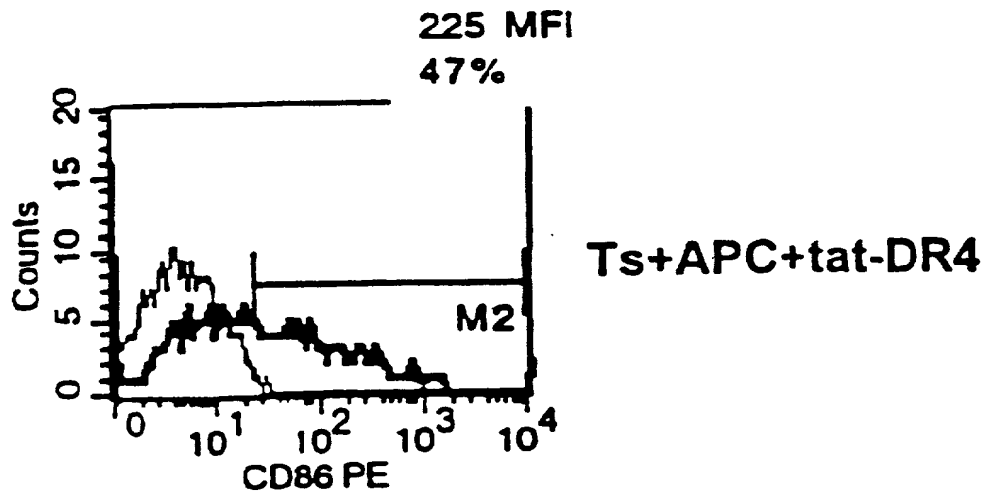


FIG. 20L

FIG. 21A

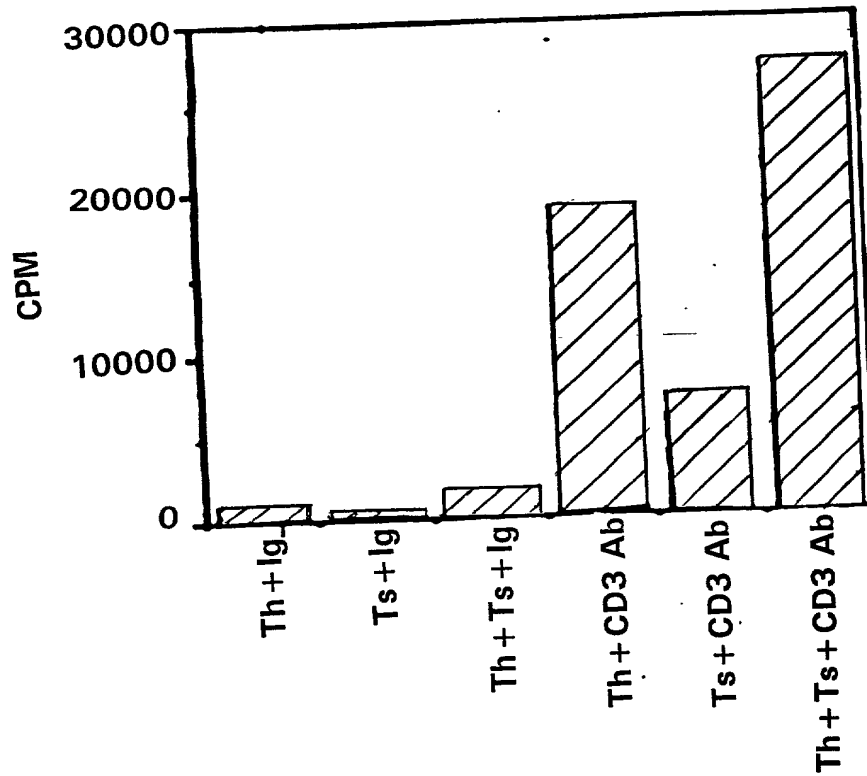


FIG. 21B

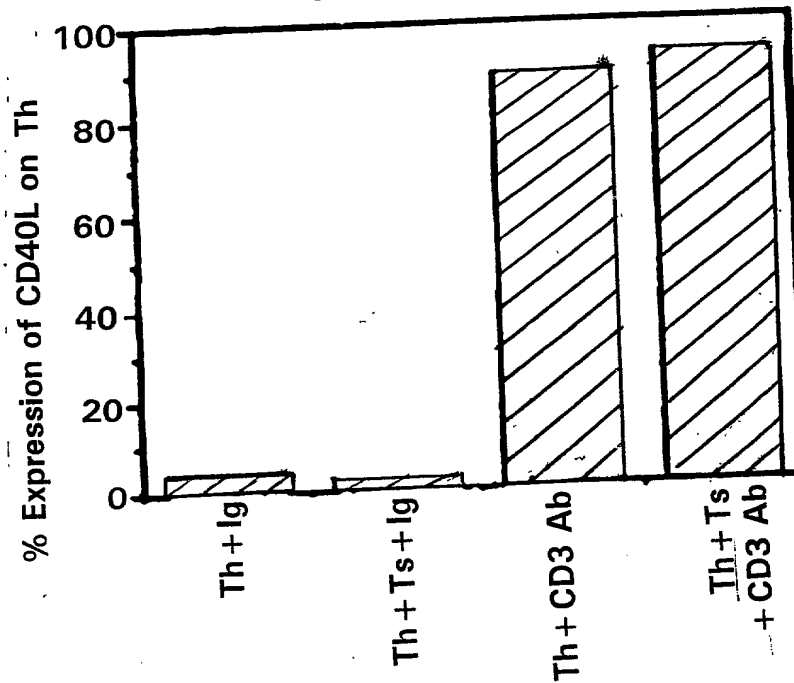


FIG. 21C

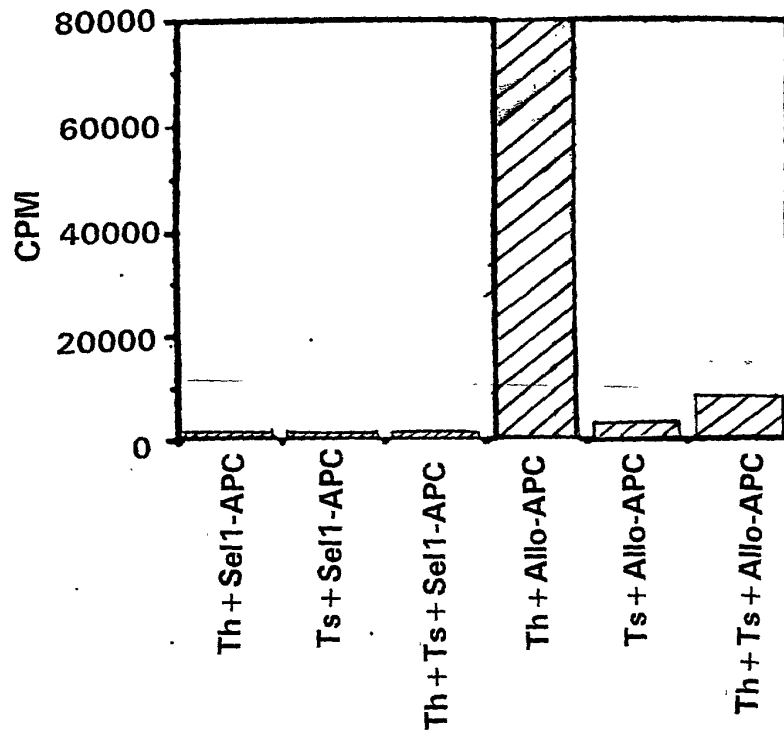
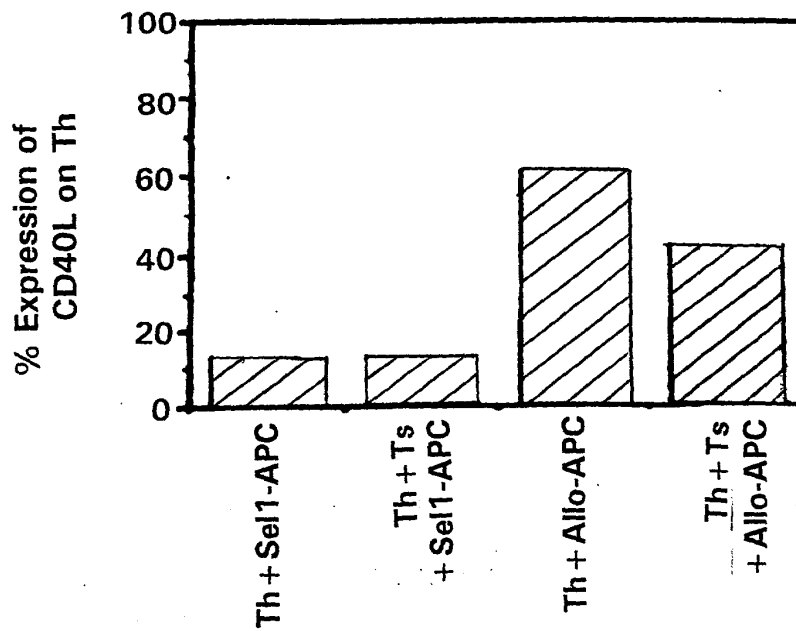
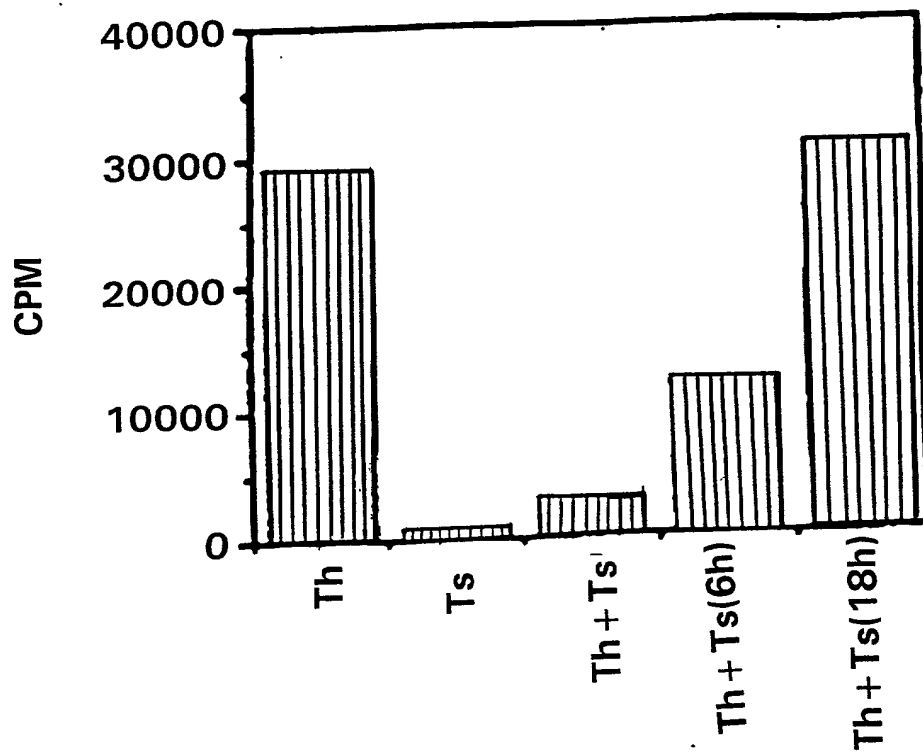


FIG. 21D



39/73

FIG. 22



00T22T"FE94/60

40/73

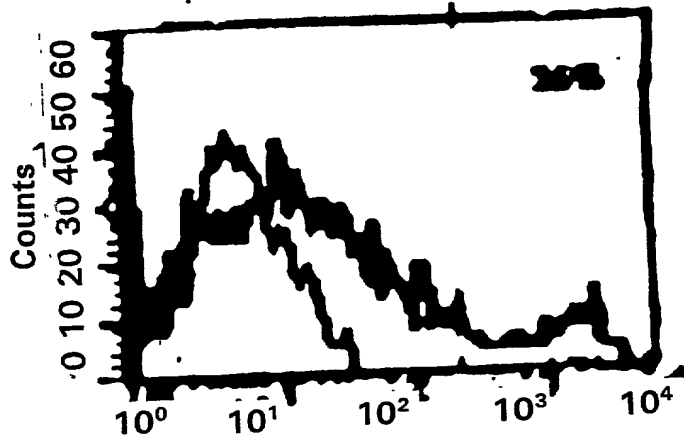


Fig. 23A-1
CD54

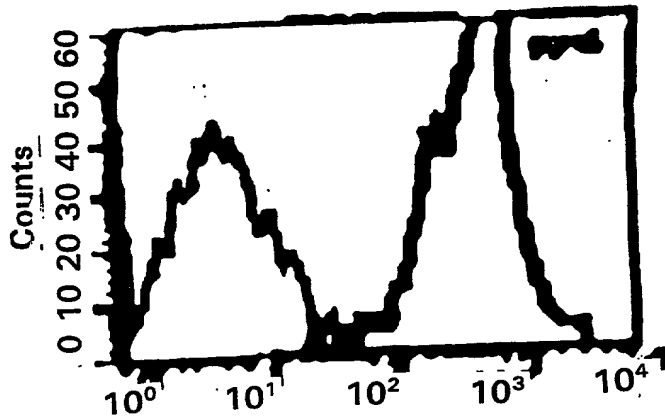


Fig. 23A-2
CD58

001221-1-1E94/260

41/73

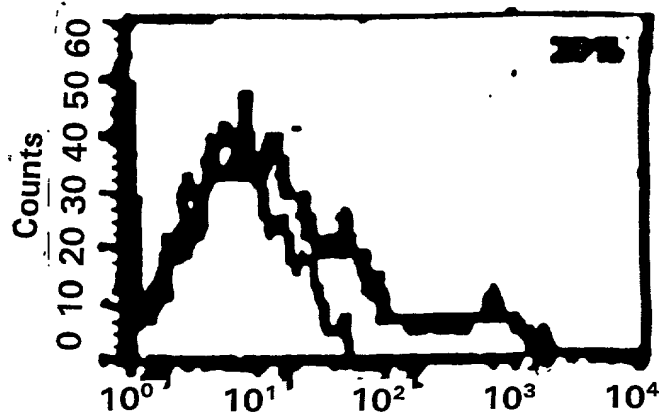


Fig. 23A-3
CD40

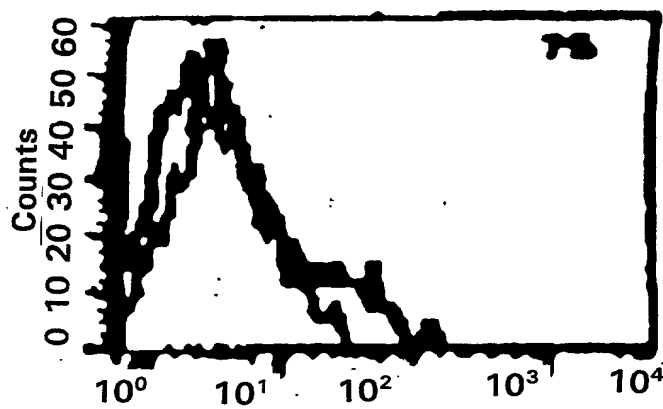


Fig. 23A-4
CD80

007007 11.09.2000

42/73

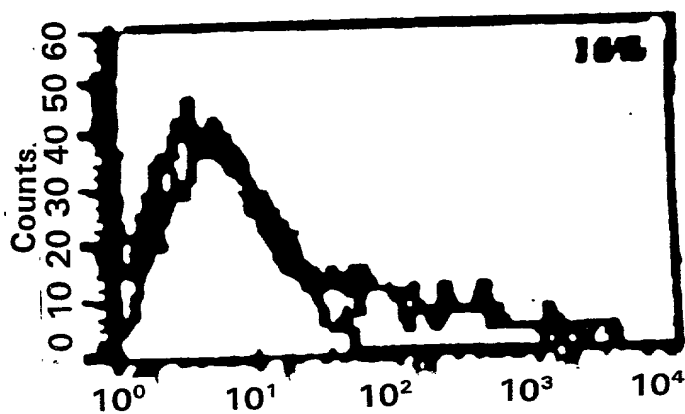


Fig. 23A-5
CD86

001221" T.E.94.60

43/73

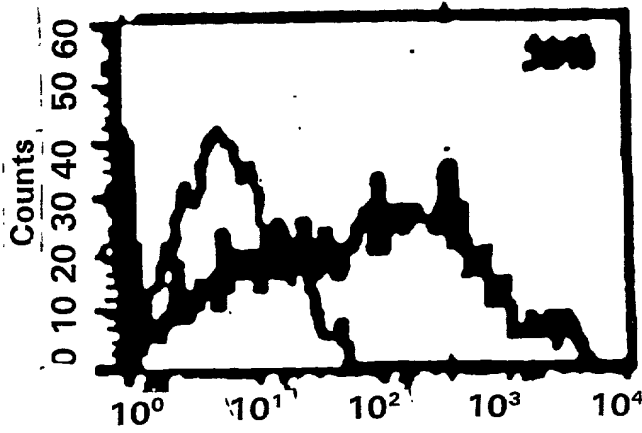


Fig. 23B-1
CD54

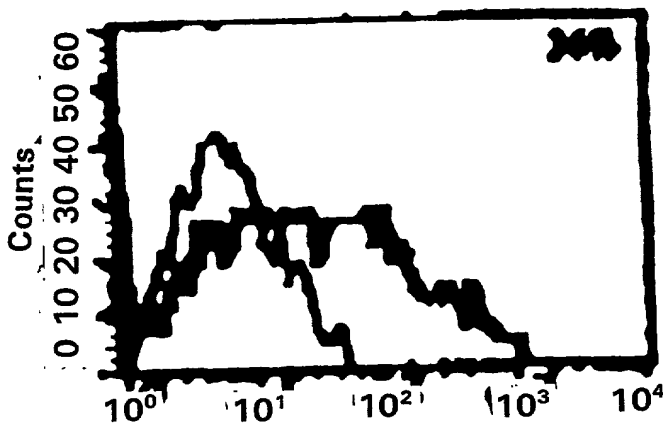


Fig. 23B-2
CD58

001221 11E9460

44/73

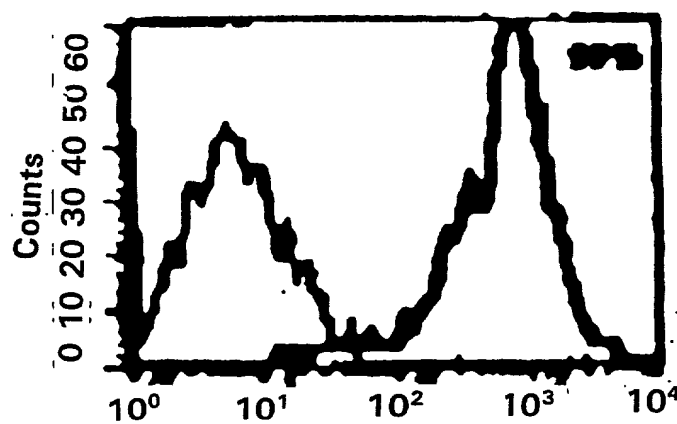


Fig. 23B-3
CD40

CD40-PE-460

45/73

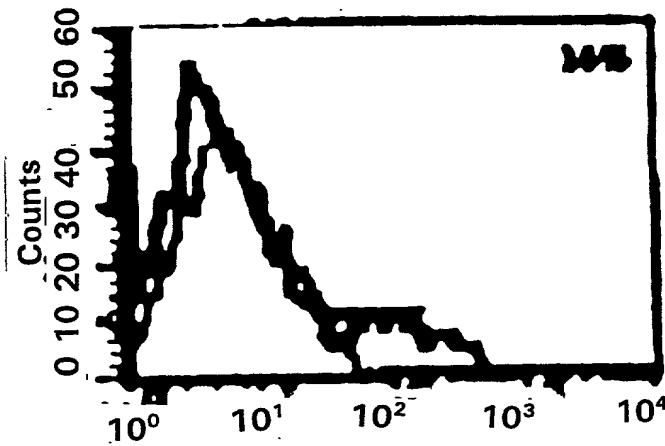


Fig. 23B-4
CD80

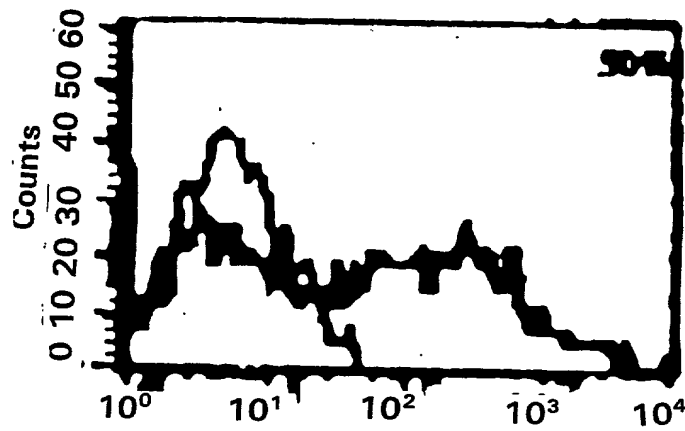


Fig. 23B-5
CD86

007227" FE94250

46/73

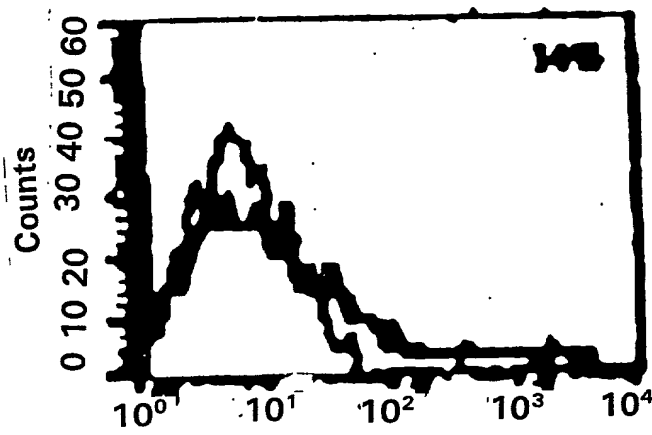


Fig. 23C-1
CD54

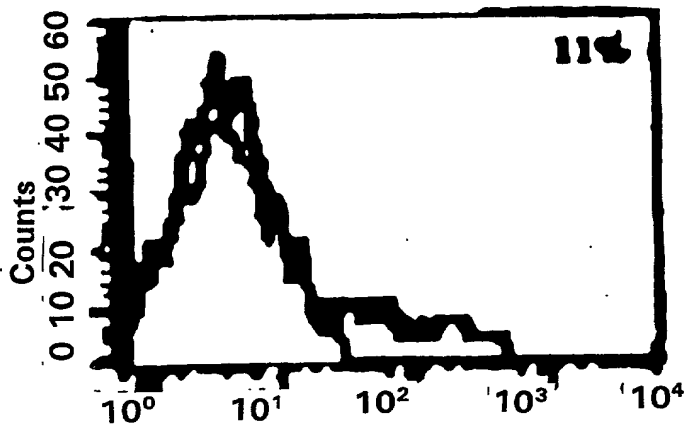


Fig. 23C-2
CD58

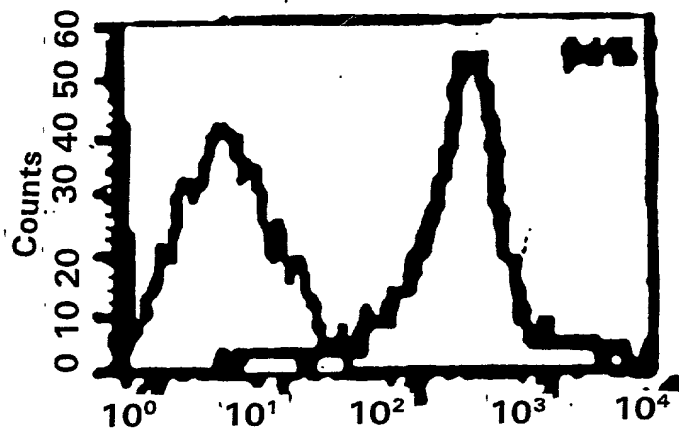


Fig. 23C-3
CD40

47/73

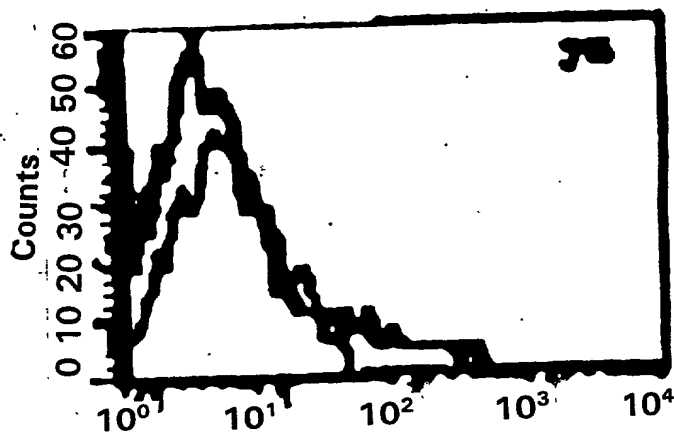


Fig. 23C-4
CD80

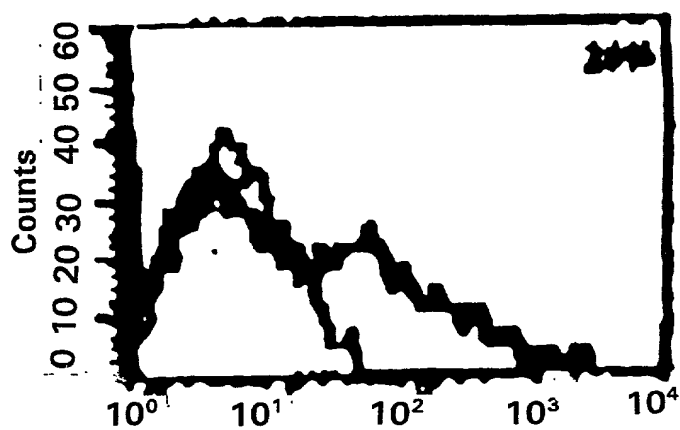


Fig. 23C-5
CD86

007227" FE 94/60

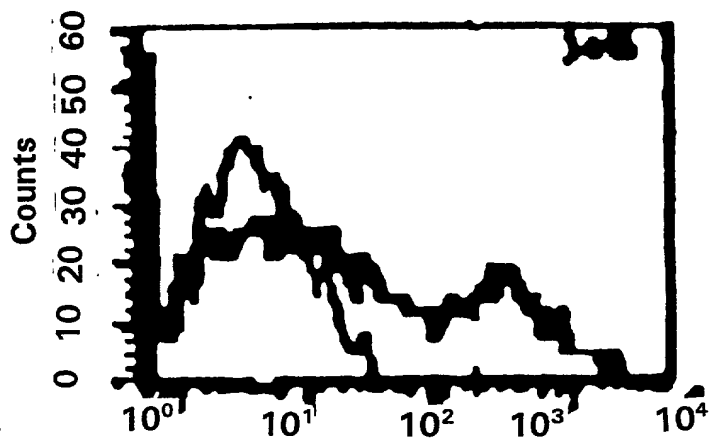
[illegible]

FIG. 23D-1
CD54

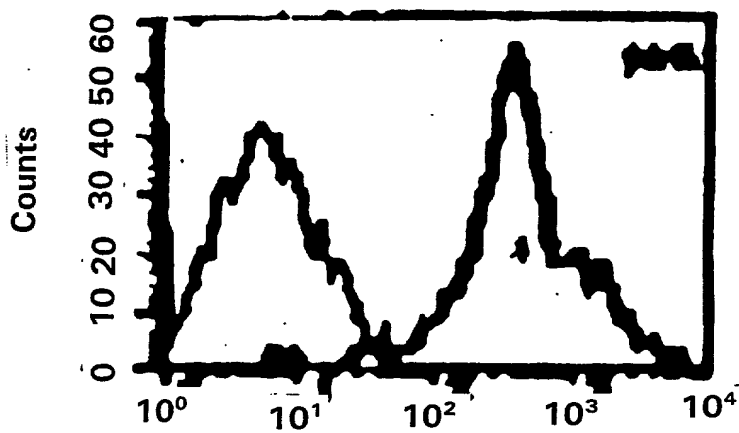
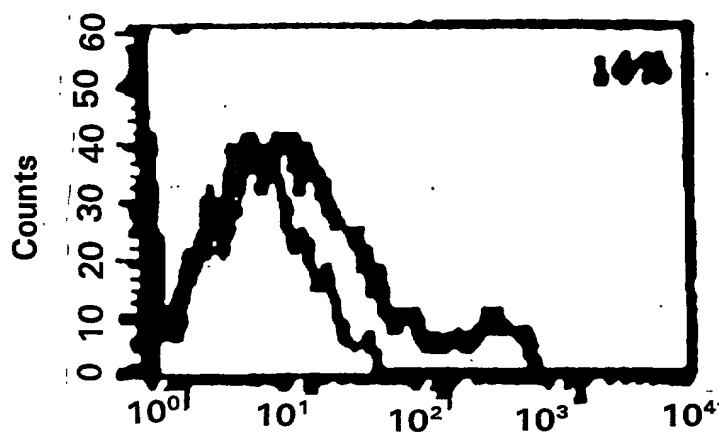
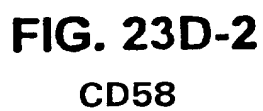


FIG. 23D-3
CD40

49/73

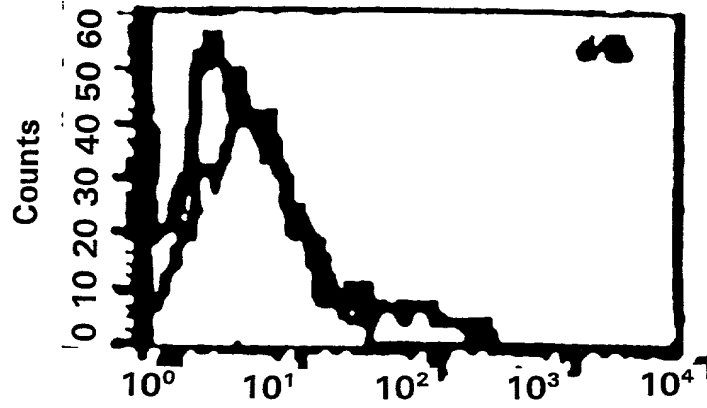


Fig. 23D-4
CD80

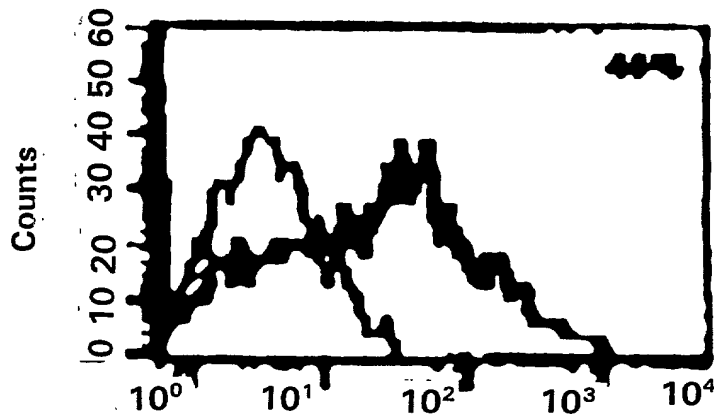


Fig. 23D-5
CD86

001221-17E94/60

[illegible]**CD54**

CD58



CD40

51/73

CD80

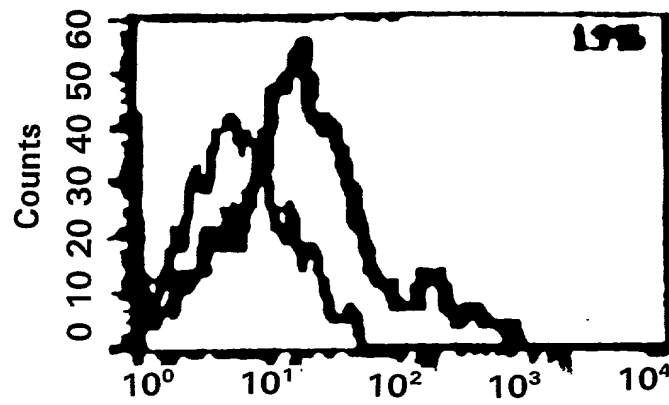


Fig. 23E-4

CD86

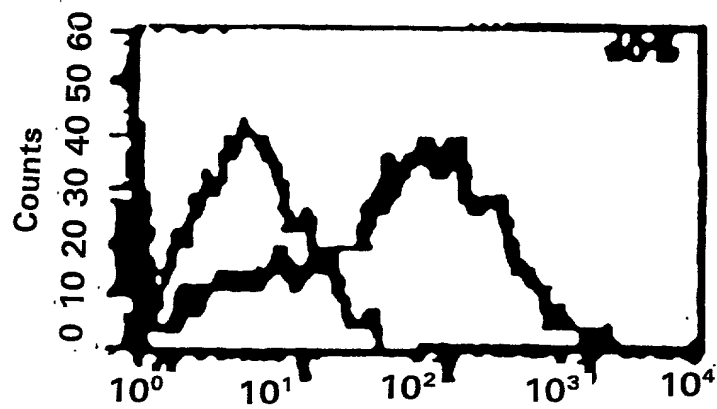


Fig. 23E-5

52/73

FIG. 24

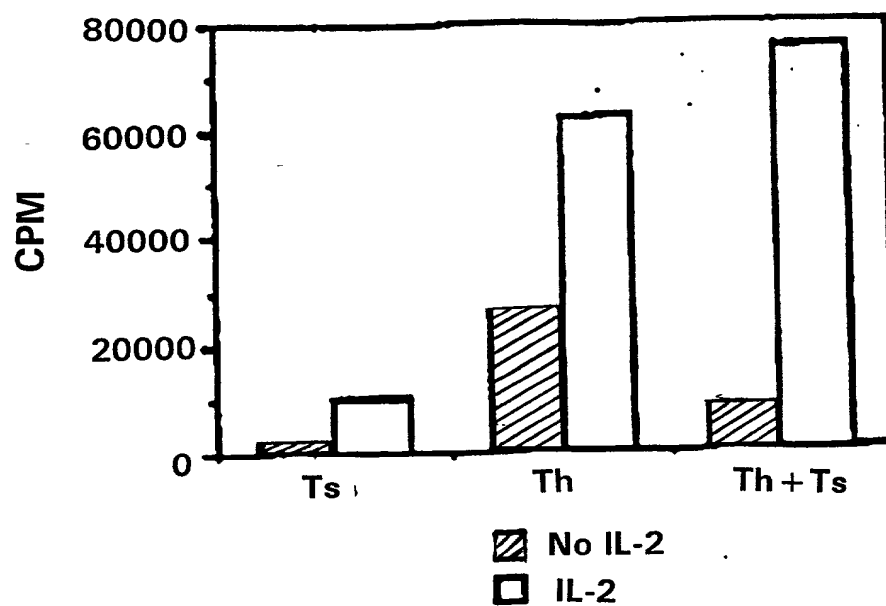
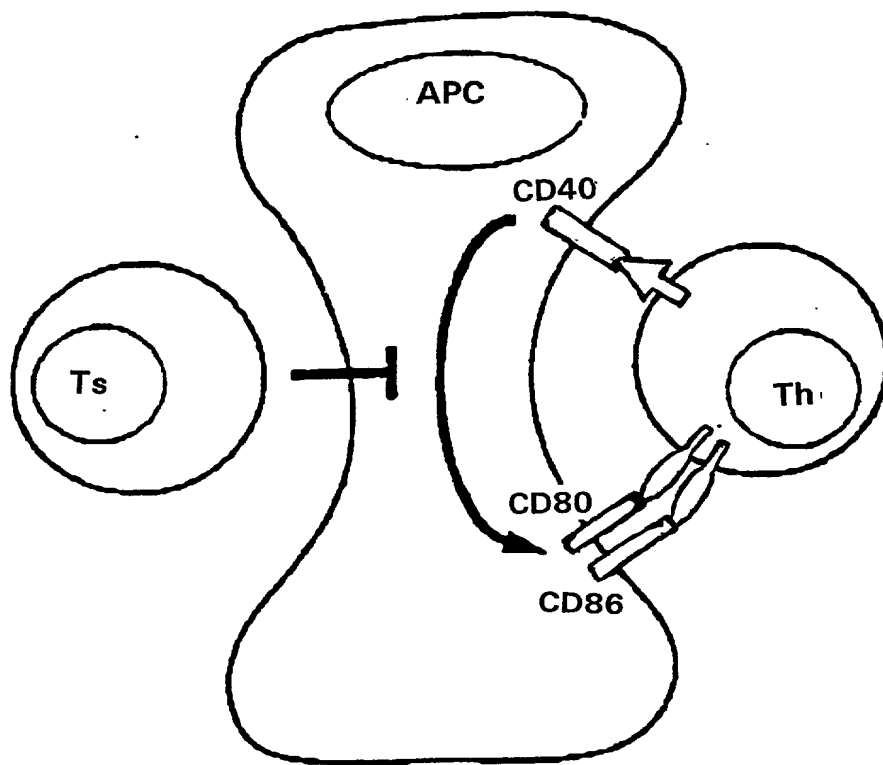


FIG. 25



HLA A, B and DR Antigen Values and Split Equivalences

A Locus	Equivalent	B Locus	Equivalent	DR Locus	Equivalent
1	1	5	5	1	1
2	2	7	7	2	2,15,16
3	3	8	8	3	3,17,18
9	9	12	12	4	4
10	10,66	13	13	5	5,11,12
11	11	14	14,64,65	6	6,13,14
19	19,74	15	15,75,76,77	7	7
23	23	16	16	8	8
24	24	17	17,58	9	9
25	25	18	18	10	10
26	26	21	21	11	11,5
28	28,68,69	22	22,54,55,56	12	12,5
29	29	27	27	13	13,6
30	30	35	35	14	14,6
31	31	37	37	15	15,2
32	32	38	38	16	16,2
33	33	39	39	17	17,3
34	34	40	40,61	18	18,3
36	36	41	41	51	51
43	43	42	42	52	52
66	66,10	44	44	53	53
68	68,23	45	45	* 103	103
69	69,23	46	46	* 1403	1403
74	74,19	47	47	* 1404	1404
80	80	48	48	** 99	99
* 203	203	49	49		
* 210	210	50	50		
* 2403	2403	51	51		
** 99	99	52	52		
		53	53		
		54	54,22		
		55	55,22		
		56	56,22		
		57	57		
		58	58,17		
		59	59		
		60	60		
		61	61,40		
		62	62		
		63	63		
		64	64,14		
		65	65,14		
		67	67		
		70	70,71,72		
		71	71,70		
		72	72,70		
		73	73		
		75	75,15		
		76	76,15		
		77	77,15		
		* 703	703		
		* 3901	3901		
		* 3902	3902		
		* 4005	4005		
		* 5102	5102		
		* 5103	5103		
		* 7801	7801		
		* 8101	8101		
		** 99	99		

Code 99 means not tested

55/73

FIG. 27A

DRB Protein Sequences - 20th March 1998 - SGE Marsh ANRI

10 20 30 40 50 60 70 80 90 100

DRB1*0101

GDTRPRFLWQLKFECHFFNGTERVRLLERCIYNQEE SVRFDSDVGEYRAVTELGRPDAEYWNSQK
DLLEQRRAAVDTYCRHNYGVGESFTVQRRVEPKVTVY

DRB1*01021 -----AV-----

DRB1*01022 *****-----

AV*****

DRB1*0103 -----I-DE-----

DRB1*0104 -----N-----V-----

DRB1*15011 -----P-R-----F-D-YF-----F-----I-A-----V-----Q-----

-

DRB1*15012 *****-P-R-----F-D-YF-----F-----I-A-----V-----

DRB1*15021 -----P-R-----F-D-YF-----F-----I-A-----Q-----

-

DRB1*15022 *****-----F-D-YF-----F-----I-A-----

DRB1*15023 *****-P-R-----F-D-YF-----F-----I-A-----

DRB1*1503 -----P-R-----F-D-HF-----F-----I-A-----V-----Q-----

DRB1*1504 *****-P-R-----F-D-YF-----F-----F-A-----V-----

DRB1*1505 *****-P-R-----F-D-YF-----F-----A-----V-----

DRB1*1506 *****-P-R-----F-D-YF-----F-A-----I-A-----V-----

DRB1*16011 -----P-R-----F-D-YF-----F-D-----Q-----

-

DRB1*16012 *****-P-R-----F-D-YF-----F-D-----

DRB1*16021 -----P-R-----F-D-YF-----D-----Q-----

DRB1*16022 *****-P-R-----F-D-YF-----D-----

DRB1*1603 -----P-R-----F-D-YF-----F-D-A-----Q-----

-

DRB1*1604 *****-P-R-----F-D-YF-----F-D-L-----

DRB1*1605 *****-P-R-----F-D-YF-----I-D-----

DRB1*1607 *****-P-R-----FPD-YF-----I-D-----

DRB1*1608 *****-P-R-----F-D-YF-----N-----F-D-----

DRB1*03011 -----EYSTS-----Y-D-YFH-----N-----F-----K-GR-N-----V-----

-H-----

DRB1*03012 *****-EYSTS-----Y-D-YFH-----N-----F-----K-GR-N-----V-----

-*****

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FIG 27B

DRB1*03021 -----EYSTS-----F-YFH-N-----K-GR-N-----
 H-----
 DRB1*03022 -----EYSTS-----F-YFH-N-----K-GR-N-----
 H-----**
 DRB1*0303 *****YSTS-----F-YFH-N-----K-GR-N-----V-----

 DRB1*0304 *****EYSTS-----Y-D-YFH-----F-----K-GR-N-----V-----

 DRB1*0305 *****EYSTS-----Y-D-YFH-N-----F-----K-GR-N-----

 DRB1*0306 *****EYSTS-----Y-D-YFH-N-----K-GR-N-----V-----

 DRB1*0307 -----EYSTS-----F-D-YFH-N-----F-----K-GR-N-----V-----
 -H-----
 DRB1*0308 -----EYSTS-----Y-D-YFH-N-----F-----E-----K-GR-N-----V-----
 -H-----
 DRB1*0309 *****EYSTS-----Y-D-YFH-R-N-----F-----K-GR-N-----

 DRB1*0310 -----EYSTS-----Y-D-YFH-N-----F-----A-H-----K-GR-N-----V-----
 -H-----
 DRB1*0311 *****EYSTS-----Y-D-YFH-N-----F-----K-GQ-N-----V-----

 DRB1*04011 -----E-V-H-----F-D-YF-H-Y-----K-----Y-----
 E-----
 DRB1*04012 *****E-V-H-----F-D-YF-H-Y-----K-----

 DRB1*0402 -----E-V-H-----F-D-YF-H-Y-----I-DE-----V-----

 DRB1*0403 -----E-V-H-----F-D-YF-H-Y-----E-----V-----Y-----
 E-----
 DRB1*0404 -----E-V-H-----F-D-YF-H-Y-----V-----Y-----
 E-----
 DRB1*04051 -----E-V-H-----F-D-YF-H-Y-----S-----

 DRB1*04052 *****E-V-H-----F-D-YF-H-Y-----S-----

 DRB1*0406 -----E-V-H-----F-D-YF-H-----E-----V-----Y-----
 E-----
 DRB1*0407 -----E-V-H-----F-D-YF-H-Y-----E-----

 DRB1*0408 *****E-V-H-----F-D-YF-H-Y-----

 DRB1*0409 *****F-D-YF-H-Y-----S-----K-----

 DRB1*0410 *****E-V-H-----F-D-YF-H-Y-----S-----V-----

 DRB1*0411 -----E-V-H-----F-D-YF-H-Y-----S-----E-----V-----Y-----
 E-----
 DRB1*0412 *****E-V-H-----F-D-YF-H-Y-----S-----I-D-L-----V-----

 DRB1*0413 *****H-----F-D-YF-H-Y-----K-----V-----

FIG. 27C

DRB1*0415 *****E-V-H-----F-D-YF-H-Y-----E-----F-D-----V-

 DRB1*0416 *****-----F-D-YF-H-Y-----Q-----K-----

 DRB1*0417 *****-----F-D-YF-H-Y-----S-----E-----

 DRB1*0418 *****-----F-D-YF-H-Y-----I-D-L-----V-----

 DRB1*0419 *****H-----F-D-YF-H-----

 DRB1*0420 *****-----F-D-YF-H-----E-----

 DRB1*0421 *****E-V-H-----F-D-YF-H-----K-----

 DRB1*0422 *****E-V-H-----F-D-YF-H-Y-----K-GR-N-----V-----

 DRB1*0423 *****E-V-H-----F-D-YF-H-Y-----V-R-----

 DRB1*0424 *****E-V-H-----F-D-YF-H-Y-----S-----R-----

 DRB1*0425 *****E-V-H-----F-D-YF-H-Y-----F-D-L-----V-----

 DRB1*0426 *****E-V-H-----F-D-YF-H-Y-----T-----K-----

 DRB1*0427 *****E-V-H-----F-D-YF-H-Y-----E-----AV-----

 DRB1*11011 -----EYSTS-----F-D-YF-----Y-----F-----E-----F-D-----
 H-----
 DRB1*11012 -----EYSTS-----F-D-YF-----Y-----F-----E-----F-D-----
 H-----
 DRB1*11013 *****EYSTS-----F-D-YF-----Y-----F-----E-----F-D-----

 DRB1*1102 -----EYSTS-----F-D-YF-----Y-----F-----E-----I-DE-----V-----
 H-----
 DRB1*1103 -----EYSTS-----F-D-YF-----Y-----F-----E-----F-DE-----V-----
 H-----
 DRB1*11041 -----EYSTS-----F-D-YF-----Y-----F-----E-----F-D-----V-----

 DRB1*11042 -----EYSTS-----F-D-YF-----Y-----F-----E-----F-D-----V-----
 H-----
 DRB1*1105 *****EYSTG-----F-D-YF-----Y-----F-----E-----F-D-----

 DRB1*1106 *****EYSTS-----F-D-YF-----Y-----F-----E-----F-D-----AV-----

 DRB1*1107 *****EYSTS-----F-D-YF-----Y-----F-----E-----K-GR-N-----V-----

 DRB1*11081 *****S-----F-D-YF-----Y-----F-----E-----D-----

 DRB1*11082 *****S-----F-D-YF-----Y-----F-----E-----D-----

 DRB1*1109 *****-----F-D-YFH-----N-----F-----E-----F-D-----

 DRB1*1110 *****-----F-D-YFH-----F-----F-----E-----F-D-----

FIG. 27D

DRB1*1111 *****S-----F-D-YF---Y-----F-----E-----F-DE-----

 DRB1*1112 *****-----F-D-YF---F-----F-----E-----F-D-----

 DRB1*1113 -----EYSTS-----F-D-YFH---F-----F-----E-----R-----V-----

 DRB1*1114 -----EYSTS-----F-D-YF---Y-----F-----E-----I-DE-----

 DRB1*1115 -----EYSTS-----F-D-YF---DL-----F-----E-----F-D-----
 H-----
 DRB1*1116 *****-EYSTS-----F-D-YFH---N-----F-----E-----I-DE-----V-----
 -*****
 DRB1*1117 -----EYSTS-----F-D-YFH---F-----E-----R-E-----V-----
 H-----
 DRB1*1118 *****-EYSTS-----F-D-YF---Y-----F-----E-----I-D-----V-----

 DRB1*1119 *****-EYSTS-----F-D-YF---Y-----F-----E-----I-D-----

 DRB1*1120 *****-EYSTS-----F-D-YFH---N-----F-----E-----I-DE-----

 DRB1*1121 *****-EYSTS-----F-D-YF---Y-----F-----E-----I-DE-----AV-----

 DRB1*1122 *****-E-V-H-----F-D-YF---Y-----F-----E-----F-D-----

 DRB1*1123 *****-EYSTS-----F-D-YF---Y-----F-----E-----F-D-L-----

 DRB1*1124 *****-EYSTS-----F-D-YF---D-----F-----E-----F-D-----

 DRB1*1125 *****-EYSTS-----F-D-YF---Y-----F-----E-----F-D-L-----V-----
 -*****
 DRB1*1126 *****-EYSTS-----F-D-YF---Y-----F-----E-----

 DRB1*1127 *****-EYSTS-----F-D-YF---Y-----F-----E-----F-D-N-----

 DRB1*1128 *****-EYSTS-----F-D-YF---N-----F-----E-----F-D-----

 DRB1*1129 *****-EYSTS-----F-D-YF-----F-----E-----F-D-----

 DRB1*1130 *****-EL-S-----F-D-YF---Y-----F-----E-----F-D-----

 DRB1*1131 -----EYSTS-----F-D-YF---Y-----F-----E-H-----I-D-----
 H-----
 DRB1*1201 -----EYSTG-Y-----HFH-LL-----F-----V-S-----I-D-----AV-----
 -H-----
 DRB1*12021 *****-EYSTG-Y-----HFH-LL-----F-----V-S-----F-D-----
 AV*****
 DRB1*12022 *****-EYSTG-Y-----HFH-LL-----F-----V-S-----F-D-----AV-----

 DRB1*12032 *****-EYSTG-Y-----HFH-LL-----F-----V-S-----I-D-----V-----
 -*****
 DRB1*1204 *****EYSTG-Y-----HFH-LL-----F-----E-----I-D-----
 AV*****
 DRB1*1205 *****-EYSTG-Y-----HFH-FL-----F-----V-S-----I-D-----AV-----

Fig. 27E

DRB1*1301 —EYSTS—F-D-YFH—N—F—I-DE—V—
 H—
 DRB1*1302 —EYSTS—F-D-YFH—N—F—I-DE—
 H—
 DRB1*13031 —EYSTS—F-D-YF—Y—S—I-DK—
 H—*
 DRB1*13032 *****EYSTS—F-D-YF—Y—S—I-DK—

 DRB1*1304 —EYSTS—F-D-YF—Y—F—S—I-DE—V—
 H—*
 DRB1*1305 *****EYSTS—F-D-YFH—N—F—F-D—

 DRB1*1306 *****F-D-YFH—N—F—I-D—V—

 DRB1*13071 *****EYSTS—F-D-YF—Y—F-D—

 DRB1*1308 *****EYSTS—F-D-YFH—F—I-DE—V—

 DRB1*1309 *****EYSTS—F-D-YFH—N—F—I-A—V—

 DRB1*1310 *****EYSTS—F-D-YFH—N—F—I-DK—V—

 DRB1*1311 *****EYSTS—F-D-YF—Y—F—F-D—V—

 DRB1*1312 *****EYSTS—F-D-YF—Y—S—I-D—

 DRB1*1313 *****EYSTS—F-D-YF—Y—S—I-D-L—

 DRB1*1314 *****TS—F-D-YF—Y—F—F-D—

 DRB1*1315 *****EYSTS—F—YFH—N—F—I-DE—V—

 DRB1*1316 *****EYSTS—F-D-YFH—N—F—I-DE—D—

 DRB1*1317 —EYSTG—Y—F-D-YF—Y—F—I-DE—V—
 H—
 DRB1*1318 *****EYSTS—F-D-YFH—N—F—F-D-L—V—

 DRB1*1319 —EYSTS—F—YFH—F—I-DE—V—H—
 —
 DRB1*1320 *****EYSTS—F-D-YFH—N—F—DE—V—

 DRB1*1321 —EYSTS—F-D-YF—Y—F—S—F-D—H—
 —
 DRB1*1322 *****EYSTS—F-D-YF—Y—F—I-DE—V—

 DRB1*1323 *****EYSTS—F-D-YF—Y—F—I-DE—

 DRB1*1324 *****EYSTS—F-D-YF—Y—F—F-DE—V—

 DRB1*1325 *****EYSTS—F-D-YF—Y—F—D—

 DRB1*1326 *****EYSTS—F—YFH—N—F-D—

007227-123400

Fig. 27F

DRB1*1327 *****-EYSTS-----Y-D-YFH-N-----F-----I-DE-----V-----

 DRB1*1328 *****-EYSTS-----F-D-YFH-N-----F-----I-DE-----R-V-----

 DRB1*1329 *****-EYSTS-----F-D-YFH-N-----F-----DE-----

 DRB1*1330 *****-EYSTS-----F-D-YF-Y-----F-----S-----I-D-----

 DRB1*1331 *****-EYSTS-----F-D-YFH-N-----F-----V-----I-DE-----

 DRB1*1332 *****-EYSTS-----F-D-YFH-N-----S-----I-DE-----V-----

 DRB1*1333 *****-EYSTS-----F-D-YF-Y-----S-----I-DK-N-----

 DRB1*1401 -----EYSTS-----F-D-YFH-F-----A-H-----R-E-----V-----

 DRB1*1402 -----EYSTS-----F-YFH-N-----

 DRB1*1403 -----EYSTS-----F-YFH-N-----D-L-----

 DRB1*1404 *****-EYSTG-Y-----F-D-YFH-F-----A-H-----R-E-----V-----

 DRB1*1405 *****-EYSTS-Q-----F-D-YFH-F-----R-E-----V-----

 DRB1*1406 *****-EYSTS-----F-YFH-N-----V-----

 DRB1*1407 *****EYSTS-----F-D-YFH-F-----A-H-----R-E-----

 DRB1*1408 *****-EYSTS-----F-D-YFH-F-----H-----R-E-----V-----

 DRB1*1409 *****-EYSTS-----F-D-YFH-N-----

 DRB1*1410 *****-E-V-H-----F-D-YFH-F-----A-H-----R-E-----V-----

 DRB1*1411 *****EYSTG-Y-----F-D-YFH-F-----E-----R-E-----
 V*****
 DRB1*1412 *****S-----F-YFH-N-----D-L-----
 V*****
 DRB1*1413 *****EYSTS-----F-YFH-N-----S-----

 DRB1*1414 *****-EYSTS-----F-D-YFH-F-----R-E-----

 DRB1*1415 *****STG-Y-----F-D-YFH-F-----F-D-L-----V-----

 DRB1*1416 *****-EYSTS-----F-D-YFH-F-----A-H-----I-DE-----V-----

 DRB1*1417 *****-EYSTS-----F-D-YFH-N-----F-----V-----

 DRB1*1418 *****EYSTS-----F-YFH-N-----R-E-----V-----

 DRB1*1419 -----EYSTS-----F-YFH-N-----K-----

 DRB1*1420 *****-EYSTS-----F-YFH-F-----V-----

FIG. 27G

DRB1*1421 *****-EYSTS-----F-D-YFH---N-----F-----K-----V-

 DRB1*1422 *****-EYSTS-----F-D-YFH---F-----A-H---F-D-----

 DRB1*1423 *****-EYSTS-----F-D-YFH---F-----R-E---V-----

 DRB1*1424 *****-EYSTS-----F-YFH---N-----I-A-----
 H-----
 DRB1*1425 *****EYSTS-----F-D-YF---Y-----A-H---F-D-----

 DRB1*1426 *****-EYSTS-----QF-D-YFH---F-----A-H---R-E---V-----
 -*****
 DRB1*1427 *****-EYSTS-----F-YFH---N-----F-D-L-----

 DRB1*1428 *****-EYSTG-Y-----F-D-YFH---F-----A-H---R-E-----
 AV*****
 DRB1*1429 *****-EYSTS-----F-YFH---N-----AV-----

 DRB1*1430 *****-EYSTS-----F-D-YFH---N-----F-----

 DRB1*1431 *****-EYSTG-Y-----F-D-YFH---F-----A-H---R-----V-----

 DRB1*0701 ---Q---G-YK-----QF-LF---F-----V-S---I-D-GQ-V-----
 H-E-----
 DRB1*0703 *****-G-YK-----QF-SLF---F-----V-S---I-D-GQ-V-----

 DRB1*0801 -----EYSTG-Y-----F-D-YF---Y-----S---F-D-L-----

 DRB1*08021 -----EYSTG-Y-----F-D-YF---Y-----F-D-L-----
 H-----
 DRB1*08022 *****-EYSTG-Y-----F-D-YF---Y-----F-D-L-----
 -H-----
 DRB1*08032 -----EYSTG-Y-----F-D-YF---Y-----S---I-D-L-----
 H-----
 DRB1*08041 -----EYSTG-Y-----F-D-YF---Y-----F-D-L---V-----
 H-----*
 DRB1*08042 *****-F-D-YF---Y-----F-D-L---V-----
 -*****
 DRB1*08043 *****-EYSTG-Y-----F-D-YF---Y-----F-D-L---V-----
 -*****
 DRB1*0805 *****-EYSTG-Y-----F-D-YF---Y-----S---F-D-----

 DRB1*0806 *****-EYSTG-Y-----F-D-YF---Y-----S---F-D-L---V-----
 -*****
 DRB1*0807 *****-EYSTG-Y-----F-D-YF---Y-----V---F-D-L-----

 DRB1*0808 *****-EYSTG-Y-----F-D-YF---Y-----A-H---F-D-L-----

 DRB1*0809 *****-Y-----F-D-YFH---F-----F-D-L-----

 DRB1*0810 *****-EYSTG-Y-----F-D-YF---Y-----S---I-D-L---V-----
 -*****
 DRB1*0811 *****-EYSTG-Y-----F-D-YF---Y-----A---F-D-L-----

FIG. 27H

DRB1*0812	*****-EYSTG-Y	F-D-YF-Y	S	I-D-L	AV

DRB1*0813	*****-EYSTG-Y	F-D-YF-Y		D-L	

DRB1*0814	*****-EYSRG-Y	F-D-YF-Y	S	I-D-L	

DRB1*0815	*****-EYSTG-Y	F-D-YF-Y	H	I-D-L	

DRB1*0816	*****-EYSTG-Y	F-D-YF-D	S	F-D-L	

DRB1*0817	*****-EYSTG-Y	F-D-YF-Y	F	S	F-D-L

DRB1*0818	*****-EYSTG-Y	F-D-YF-Y	S	I-D	

DRB1*0819	*****-EYSTG-Y	F-D-YF-Y	I	I-D-L	

DRB1*09012	Q-K-D	Y-H-G-N	V-S	F-R-E-V	
H-E					
DRB1*1001	EEV	RVH-YA-Y	R	Q	

Class II and III genes
Hsp70, TGF and LTR
Colony, vpr-180A
and phosphatase

ABC transporter genes
Genes of unknown function
CYP + C
Class I genes

64/73

FIG. 29

	1					50
Sladra-0102	-----	-----	-----	-----	-----	-----
Sladra-0202	-----	-----	-----	-----	-----	-----
Sladra-0203	-----	-----	-----	-----	-----	-----
Sladra-0101	-----	-----	-----	-----	-----	-----
Sladra-02011	-----	-----	-----	-----	-----	-----
Sladra-02012	-----	-----	-----	-----	-----	-----
Consensus	VENHVIIQAE	FYLSPDKSGE	FMFDFDGDEI	FHVDMEKRET	VWRLEEFQHF	
	51					100
Sladra-0102	-----	-----	-----	-----	-----	-----
Sladra-0202	-----	-----	-m-----	-----	-----	-----
Sladra-0203	-----	-----	-----	-----	-----	-----
Sladra-0101	-----	-----	-----	-----	-----	-----
Sladra-02011	-----	-----	-m-----	-----	-----	-----
Sladra-02012	-----	-----	-m-----	-----	-----	-----
Consensus	ASFEAQGALA	NIAVDKANLE	ILIKRSNNTP	NTNVPPEVTV	LSDKPVELGE	
	101					150
Sladra-0102	-----	-----	-----	-----	-----	-----
Sladra-0202	-----	-----	-----	-----	-----	-----
Sladra-0203	-----	-----	-----	-----	-----	-----
Sladra-0101	-----	-----	-----	-----	-----	-----
Sladra-02011	-----	-----	-----	-----	-----	-----
Sladra-02012	-----	-----	-----	-----	-----	-----
Consensus	PNILICFIDK	FSPPVVNVTV	LRNGSPVTRG	VSETVFLPRE	DHLFRKFHYL	
	151					200
Sladra-0102	-----	-----	-----	-r-----	-----	-----
Sladra-0202	-----	-----	-----	-----	-----	-----
Sladra-0203	-----	-----	-----	-----	-----	-----
Sladra-0101	-----	-----	-----	-----	-----	-----
Sladra-02011	-----	-----	-----	-----	-----	-----
Sladra-02012	-----	-----	-----	-----	-----	-----
Consensus	PFMPSTEDVY	DCQVEHWGLD	KPLLKHWFE	AQTPLPETTE	NTVCALGLIV	
	201					228
Sladra-0102	-----	-----	-----	-----	-----	-----
Sladra-0202	-----	-----	---h---	-----	-----	-----
Sladra-0203	-----	-----	---h---	-----	-----	-----
Sladra-0101	-----	-----	-----	-----	-----	-----
Sladra-02011	-----	-----	-----	-----	-----	-----
Sladra-02012	-----	-----	-----	-----	-----	-----
Consensus	ALVGIIVGTV	LIKGVKGN	ATERRGPL			

Group 01 has a leucine at residue 72 and Group 02 has a methionine.
No other polymorphisms have been found in the alpha 1 domain.

Amino Acid Sequences of SLA DRA Alleles

65/73

FIG. 30

	1	2A	4A	50
Sladrb-T	--iaq--ffm g-s-----	-----y-qky l-----	-----l-f--	
Sladrb-N	-----f- g-a-----	-----d-y f--d-y--	-----f-e-	
Sladrb-M	-----f- g-----	-----q-----	-----	
Sladrb-Z	-----y- -----	-----y-----	-----	
Sladrb-AD	-----	-----l--	-----	
Sladrb-C	--i-----q -----	-----q-n c---y--	-----	
Sladrb-WX	-----v-h-r--	-----l--d-y f-----	-----f--	
Sladrb-Y	--i----ffm g-s-----	-----y-lky l-----	-----l---e-	
Consensus	RDTPPHFLHL LKFECHFFNG	TERVLLERQ YYNGEEFVRF	DSDVGEYRAV	
	51	6A	8A	100
Sladrb-T	-----m-- k--v-----	-----	-----	
Sladrb-N	--f----- fm-- k-----v--	-----e-e--	-----r--	
Sladrb-M	-----n y-----	-----ts--	-----r--	
Sladrb-Z	-----v--d -----	-----ts--	-----r--	
Sladrb-AD	-----d -----	-----	-----	
Sladrb-C	-----r-----	-----a-----	-----	
Sladrb-WX	-----i--d s--s-----i	-----	-----	
Sladrb-Y	-----ek-----	-----gvs-s-	-----	
Consensus	TELGRPDACY WNSQKDLLEQ	RRAEVDTYCR HNYRILDTEL	VPRAEPTVT	
	101			150
Sladrb-T	-----	-----	-----	
Sladrb-N	-----	-----	-----	
Sladrb-M	-----	-----	-----	
Sladrb-Z	-----	-----	-----	
Sladrb-AD	-----	-----	-----	
Sladrb-C	-----	-----	-----	
Sladrb-WX	-----	-----	-----	
Sladrb-Y	-----	-----	-----	
Consensus	VYPAKTQPLQ HHNLLVCSVT	GFYPGHVEVR WFRNGQEEAA	GVVSTGLIPN	
	151			200
Sladrb-T	-----	-----	-----	
Sladrb-N	-----	-----t-----	-----	
Sladrb-M	-----	-----	-----	
Sladrb-Z	-----	-----	-----	
Sladrb-AD	-----	-----	-----	
Sladrb-C	-----	-----	-----	
Sladrb-WX	-----	-----	-----	
Sladrb-Y	-----	-----	-----	
Consensus	GDWTFQTMVM LETVPQSGEV	YSCRVEHPSL TSPVTVEWRA	RSESAQGM	
	201		237	
Sladrb-T	--v-----	-----	-----	
Sladrb-N	-----	-----	-----	
Sladrb-M	-----	-----	-----	
Sladrb-Z	--v-----	-----	-----	
Sladrb-AD	-----	-----	-----	
Sladrb-C	--v-----	-----	-----	
Sladrb-WX	-----	-----	-----	
Sladrb-Y	--v-----	-----	-----	
Consensus	SGIGGFVLGL LFVAVGLFIY	FKNOKGRPAL QPTGLLS		

Amino Acid Sequence of SLA-DRB Alleles

00245311.122100

66/73

FIG. 31

					50
Sladqa-02021	1	-----	-----	-----g	-----
Sladqa-02022		-----	-----	-----g	-----
Sladqa-02023		-----	-----	-----g	-----
Sladqa-0201		-----	-----	-----	-----
Sladqa-0101		-----	-r-----	-q-----	-----r--
Sladqa-0103		-----	-r-f-----	-q-----	-----r--
Sladqa-0102		-----	-f-----	-----	-----r--
Consensus		EDIAADHVAS	YGLNVYQSYG	PSGYTTFEFD	GDEEFYVDLE KKETVWQLPL
					100
Sladqa-02021	51	-----r-----	-----	-----	-----
Sladqa-02022		-----r-----	-----	-----	-----
Sladqa-02023		-----r-----	-----	-----	-----
Sladqa--201		-----	-----	-----	-----
Sladqa-0101		--e-----	-----1-	-----vt--	-----k--s--
Sladqa-0103		--e-----	-----1-	-----vt--	-----k--s--
Sladqa-0102		--e-----	-----1-	-----vt--	-----s--
Consensus		FSKFTSFDPQ	GALRNIATAK	HNLNILIKRS	NNTAAVNQVP EVTVFPPKSPV
					150
Sladqa-02021	101	-----	-----	-----	-----
Sladqa-02022		-----	-----	-----	-----
Sladqa-02023		-----	-----	-----	-----
Sladqa-0201		-----	-----	-----	-----
Sladqa-0101		i-----	-----s-----	-----	-----k-----
Sladqa-0103		i-----	-----s-----	-----	-----k-----
Sladqa-0102		i-----	-----s-----	-----	-----k-----
Consensus		MLGQPNTLIC	HVDNIFPPVI	NITWLKNGHS	VTEGFSETSF LSKNDHSFLK
					200
Sladqa-02021	151	-----	-----	-----	-----
Sladqa-02022		-----	-----	-----	-----
Sladqa-02023		-----	-----	-----	-----
Sladqa-0201		-----	-----	-----	-----
Sladqa-0101		-----	-----	-----	-----
Sladqa-0103		-----	-----	-----	-----
Sladqa-0102		-----	-----	-----	-----
Consensus		ISYLTFLPSD	DDFYDCKVEH	WGLDKPLLKH	WEPEIPAPMS ELTETVVCAL
					232
Sladqa-02021	201	-----	-----	-----	-----
Sladqa-02022		-----	-----	-----	-----
Sladqa-02023		-----	-----	-----	-----
Sladqa-0201		-----	-----	-----	-----
Sladqa-0101		-----	-----	-----	-----
Sladqa-0103		-----	-----	-----	-----
Sladqa-0102		-----	-----	1-----	-----
Consensus		GLIVGLVGIV	VGTVFIIQGL	RSGGFSRHOG	SL

Group 01 is 231 amino acids (deletion at 132) and Group 02 is 232 amino acids

Amino Acid Sequences of SLA-DQA Alleles

67/73

FIG. 32

	1				50
Sladqb-D	-----v	---g---y-	-----ws-d-	-----fl-	-----m-y--
Sladqb-D2	-----f	---g---y-	-----ws-d-	-----fl-	-----m-y--
Sladqb-XA	-----	-----	-----g--	wv-----	-----
Sladqb-Z	-----	-----y-	-----l--	wv--r--	-----
Sladqb-W	-----	-----	-----l-t-	-----ya-	-----y--
Sladqb-T	-----	-----	-----llt-	-----	-----n-y--
Sladqb-Y	-----	---g---	-----h-t-	-----	-----
Sladqb-C	-----f	---g---y-	-----g--	-----l-	-----
Consensus	GRDSPQDFVY	QFKFECYFFN	GTQRVR-VAR	YIYNQEEHVR	FDSDVGEFRA
	51				100
Sladqb-D	-----	-l---ea--	-----	-----	-----
Sladqb-D2	-----	-l---ea--	-----	-----	-----
Sladqb-XA	-----t--	-----	-----v---	-----	-----
Sladqb-Z	-----	-----e--	-----	-----	-----
Sladqb-W	-----a--	---s---i--	-t-----	-----	-----
Sladqb-T	-----	-----	-t-----	-----	-----
Sladqb-Y	-----	-----f--	-t-----	-----	-----
Sladqb-C	-----e--	s--s---	-m---v-r-	-----	-----
Consensus	VTPLGRPDAD	YWNGQKDVLE	QKRAELDTVC	KHNYQIEEGT	TLQRRVQPTV
	101				150
Sladqb-D	-----	-----	-----	-----	-----
Sladqb-D2	-----	-----	-----	-----	-----
Sladqb-XA	-----	-----	-----	-----	-----
Sladqb-Z	-----	-----	-----	-----	-----
Sladqb-W	-----	-----	-----	-----	-----
Sladqb-T	-----	-----	-----	-----	-----
Sladqb-Y	-----	-----	-----	-----	-----
Sladqb-C	-----	-----	-----	-----	-----
Consensus	TISPSKAEAL	NHHNLLVCAV	TDFYPSQVKV	QWFRNGQEET	AGVVSTPLIR
	151				200
Sladqb-D	-----	-----	-----	-----	-----
Sladqb-D2	-----	-----	-----	-----	-----
Sladqb-XA	-----	-----	-----	-----n-----	-----
Sladqb-Z	-----	-----	-----	-----	-----
Sladqb-W	-----	-----	-----	-----	-----
Sladqb-T	-----	-----	-----	-----	-----
Sladqb-Y	-----	-----	-----	-----	-----
Sladqb-C	-----	-----	-----	-----n-----	-----
Consensus	NGDWTYQVLV	MLEMNLQRGD	VYTCRVEHSS	LQSPILVEWR	AQSESAQSKM
	201		230		
Sladqb-D	-----	-----	-----	-----	-----
Sladqb-D2	-----	-----	-----	-----	-----
Sladqb-XA	-----	-----	-----	-----	-----
Sladqb-Z	-----	-----	-----	-----	-----
Sladqb-W	-----	-----	-----	-----	-----
Sladqb-T	-----	-----	-----	-----	-----
Sladqb-Y	-----	-----	-----	-----	-----
Sladqb-C	-----	-----	-----	-----	-----
Consensus	LSGVGGFVLG	LIFLGLGLFI	RHRSQKGLVR		

Amino Acid Sequences of SLA-DQB Alleles

0946344 12400

Figure 33

Nucleotide and Amino Acid Sequences of ILT3

```

1  atgatccccaccttcacggctctgctctgcctcgggctgagtctg
   M I P T F T A L L C L G L S L
46  ggccccaggaccacatgcaggcagggccctcccaaaccacc
   G P R T H M Q A G P L P K P T
91  ctctgggctgagccaggctctgtgatcagctgggggaactctgtg
   L W A E P G S V I S W G N S V
136 accatctggtgtcaggggaccctggaggctcgggagtaccgtctg
   T I W C Q G T L E A R E Y R L
181 gataaagaggaaagcccagcaccctgggacagacagaaccactg
   D K E E S P A P W D R Q N P L
226 gagcccaagaacaaggccagattctccatcccatccatgacagag
   E P K N K A R F S I P S M T E
271 gactatgcaggagataaccgctgttactatcgagccctgtaggc
   D Y A G R Y R C Y Y R S P V G
316 tggtcacagcccagtgacccctggagctggtgatgacaggagcc
   W S Q P S D P L E L V M T G A
361 tacagtaaaccacccctttcagccctgccgagtcctctgtgacc
   Y S K P T L S A L P S P L V T
406 tcaggaaagagcgtgaccctgctgtgtcagtcacggagcccaatg
   S G K S V T L L C Q S R S P M
451 gacactttccttctgatcaaggagcgggcagcccatcccctactg
   D T F L L I K E R A A H P L L
496 catctgagatcagagcacggagctcagcagcaccaggctgaattc
   H L R S E H G A Q Q H Q A E F
541 cccatgagtcctgtgacctcagtgacggggggacctacagggtgc
   P M S P V T S V H G G T Y R C
586 ttcagctcacacggcttctcccactacctgtgtcacaccccagt
   F S S H G F S H Y L L S H P S
631 gacccctggagctcatagtctcaggatccttggagggtcccagg
   D P L E L I V S G S L E G P R
676 ccctcaccacaaaggctcgtctcaacagctgcaggccctgaggac
   P S P T R S V S T A A G P E D
721 cagccctcagtcctacagggtcagtcacccacagtggtctgaga
   Q P L M P T G S V P H S G L R
766 aggcactgggaggtactgatcggggtcttgggtgtctccatcctg
   R H W E V L I G V L V V S I L
811 cttctctccctcctccttctcctcctccaacactggcgctcag
   L L S L L L F L L L Q H W R Q
856 ggaaaacacaggacattggcccagagacaggctgatttccaacgt
   G K H R T L A Q R Q A D F Q R
901 cctccaggggctgccgagccagagcccaaggacgggggcctacag
   P P G A A E P E P K D G G L Q
946 aggaggtccagcccagctgctgacgtccaggagaaaaacttctgt
   R R S S P A A D V Q G E N F C
991 gctgccgtgaagaacacacagcctgaggacgggtggaaatggac
   A A V K N T Q P E D G V E M D
1036 actcggagccacacagatgaagaccccgagcagtgacgtatgcc
   T R S P H D E D P Q A V T Y A
1081 aagggtgaacactccagacctaggagagaaatggcctctcctccc
   K V K H S R P R R E M A S P P
1126 tccccactgtctggggaattcctggacacaaaggacagacaggca
   S P L S G E F L D T K D R Q A
1171 gaagaggacagacagatggacactgaggctgctgcatctgaagcc
   E E D R Q M D T E A A A S E A
1216 ccccgagatgtgacctacgccagctgcacagctttaccctcaga
   P Q D V T Y A Q L H S F T L R
1261 cagaaggcaactgagcctcctccatcccaggaaggggcctctcca
   Q K A T E P P P S Q E G A S P
1306 gctgagcccagtgctatgccactctggccatccactaa 1344
   A E P S V Y A T L A I H *

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69/73

Figure 34A

Nucleotide and Amino Acid Sequences of *ILT4*

1 atg acccccatcgtcacagtcctgatctgtctcgggctgagtcctg
M T P I V T V L I C L G L S L
46 ggccccaggaccgcgctgcagacagggaccatccccaagcccacc
G P R T R V Q T G T I P K P T
91 ctgtgggctgagccagactctgtgatcaccaggggagtcctcgtc
L W A E P D S V I T Q G S P V
136 accctcagttgtcaggggagccttgaagcccaggagtaccgtcta
T L S C Q G S L E A Q E Y R L
181 tataggggagaaaaaatcagcatcttggattacacggatacagacca
Y R E K K S A S W I T R I R P
226 gagcttgtgaagaacggccagttccacatcccatccatcacctgg
E L V K N G Q F H I P S I T W
271 gaacacacagggcgatatggctgtcagtattacagccgcgctcgg
E H T G R Y G C Q Y Y S R A R
316 tggctctgagctcagtgacccccctgggtgctgggtgatgacaggagcc
W S E L S D P L V L V M T G A
361 taccctaaacccaccctctcagcccagcccagccctgtgggtgacc
Y P K P T L S A Q P S P V V T
406 tcaggaggaaggggtgacccctccagtggtgagtcacagggtggcattt
S G G R V T L Q C E S Q V A F
451 ggcggttctattctgtgtaaggaaggagaagatgaacacccacaa
G F I L C K E G E D E H P Q
496 tgccctgaactcccagccccatgcccgtgggtcgtcccgcgccatc
C L N S Q P H A R G S S R A I
541 ttctccgtgggccccgtgagcccgaatcgaggtgggtcgacaggg
F S V G P V S P N R R W S H R
586 tgctatggttatgacttgaactctccctatgtgtgggtcttcaccc
C Y G Y D L N S P Y V W S S P
631 agtgatctcctggagctcctgggtcccaggtgtttctaagaagcca
S D L L E L L V P G V S K K P
676 tcactctcagtgacagccgggtcctgtcatggcccctggggaaagc
S L S V Q P G P V M A P G E S
721 ctgacctccagtggtgtctctgatgtcggtatgacagatttgtt
L T L Q C V S D V G Y D R F V
766 ctgtacaaggaggggggaacgtgaccttcgccagctccctggccgg
L Y K E G E R D L R Q L P G R
811 cagccccaggctgggtctctcccaggccaacttcaccctgggcccct
Q P Q A G L S Q A N F T L G P
856 gtgagccgctcctacgggggccaagtacagatgctacgggtgcacac
V S R S Y G G Q Y R C Y G A H
901 aacctctcctctgagtgctcgccccccagcgacccccctggacatc
N L S S E C S A P S D P L D I
946 ctgatcacaggacagatccgtggcacacccttcattctcagtgacg
L I T G Q I R G T P F I S V Q
991 ccaggccccacagtgccctcaggagagaacgtgacccctgctgtgt
P G P T V A S G E N V T L L C
1036 cagtcatggcggcagttccacactttccttctgaccaaggcgga
Q S W R Q F H T F L L T K A G
1081 gcagctgatgccccactccgtctaagatcaatacacgaatatcct
A A D A P L R L R S I H E Y P
1126 aagtaccaggctgaattcccatgagtcctgtgacctcagcccac
K Y Q A E F P M S P V T S A H
1171 gcggggacctacaggtgctacgggtcactcaactccgaccctac
A G T Y R C Y G S L N S D P Y

094631.122100

Figure 34B

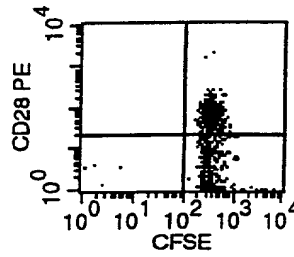
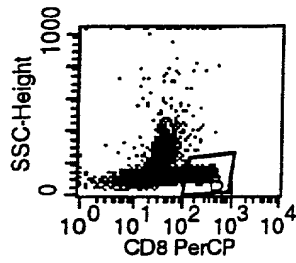
1216 ctgctgtctcaccgccagtgagcccctggagctcgtggtctcagga
L L S H P S E P L E L V V S G
1261 ccctccatgggttccagccccccaccacgggtcccatctccaca
P S M G S S P P P T G P I S T
1306 cctggccctgaggaccagcccctcaccgccactgggtcggatccc
P G P E D Q P L T P T G S D P
1351 caaagtgggtctgggaaggcacctgggggttgatcggtcgtcttg
Q S G L G R H L G V V I G I L
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1441 atcctccgacatcgacgtcagggcaaactggacatcgacccag
I L R H R R Q G K H W T S T Q
1486 agaaaggctgatttccaacatcctgcaggggctgtggggccagag
R K A D F Q H P A G A V G P E
1531 cccacagacagaggcctgcagtggaggtccagcccagctgccgac
P T D R G L Q W R S S P A A D
1576 gcccaggaagaaaacctctatgctgccgtgaaggacacacagcct
A Q E E N L Y A A V K D T Q P
1621 gaagatgggggtggagatggacactcgggctgctgcatctgaagcc
E D G V E M D T R A A A S E A
1666 ccccaggatgtgacctacgccagctgcacagcttgaccctcaga
P Q D V T Y A Q L H S L T L R
1711 cggaaggcaactgagcctcctccatcccaggaagggaacctcca
R K A T E P P P S Q E R E P P
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A E P S I Y A T L A I H *

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71/73

Figure 35

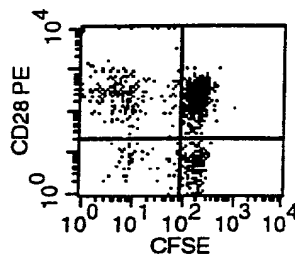
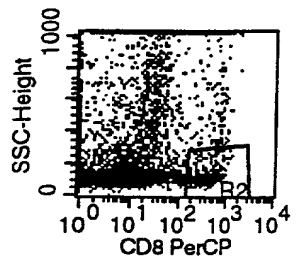
DAY 0



Gate: G1

Quad	Events	% Gated	X Mean
UL	0	0.00	***
UR	439	56.79	350.95
LL	4	0.52	2.80
LR	330	42.69	482.99

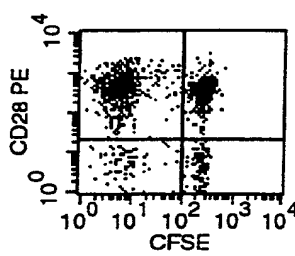
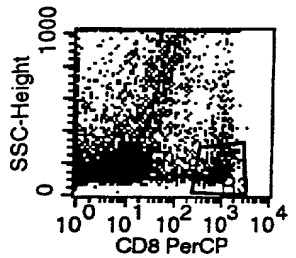
DAY 5



Gate: G2

Quad	Events	% Gated	X Mean
UL	214	13.70	14.01
UR	1134	72.60	202.84
LL	45	2.88	26.18
LR	169	10.82	190.79

DAY 7



Gate: G3

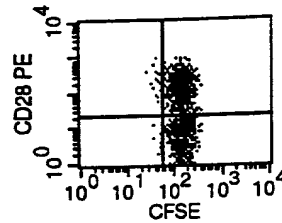
Quad	Events	% Gated	X Mean
UL	2290	38.33	9.23
UR	2973	49.77	273.42
LL	261	4.37	12.50
LR	450	7.53	242.13

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72/73

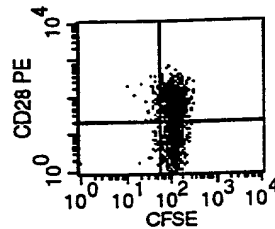
Figure 36

0 HR



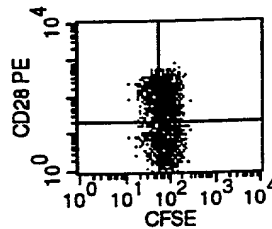
Quad	Events	% Gated	X Mean
UL	18	1.36	40.96
UR	737	55.62	143.24
LL	10	0.75	47.01
LR	560	42.26	151.29

48 HR
+APC



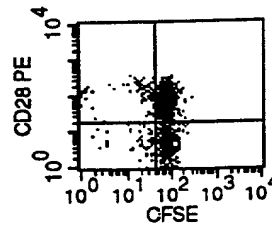
Quad	Events	% Gated	X Mean
UL	53	2.86	42.38
UR	1212	65.48	122.49
LL	23	1.24	41.38
LR	563	30.42	121.41

48 HR
+APC+IL2



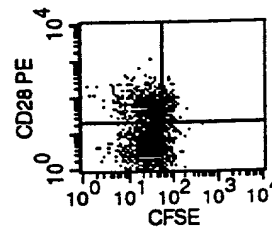
Quad	Events	% Gated	X Mean
UL	645	19.00	39.93
UR	1382	40.72	95.07
LL	311	9.16	40.05
LR	1056	31.11	101.61

72 HR
+APC



Quad	Events	% Gated	X Mean
UL	114	9.19	27.62
UR	711	57.34	78.27
LL	57	4.60	24.32
LR	358	28.87	83.25

72 HR
+APC+IL2



Quad	Events	% Gated	X Mean
UL	2911	30.97	28.62
UR	717	7.63	76.38
LL	4965	52.83	29.50
LR	805	8.57	74.95

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73/73

Figure 37

